

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 17:38:03 ; Search time 130.923 Seconds
(without alignments)
13025.213 Million cell updates/sec

Title: US-10-713-381-1_COPY_1179_1208
Perfect score: 30
Sequence: 1 catgctgttcaaccgttcgtctgttcca 30

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sv.*
12: gb_un.*
13: gb_vi.*
14: gb_brg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	30	100.0	30	6	AX224397	Sequence
2	30	100.0	255	6	AX224402	Sequence
3	30	100.0	1394	6	BD062176	Male tiss
4	30	100.0	1394	6	BD062177	Male tiss
5	30	100.0	1394	6	AX224394	Sequence
6	30	100.0	1394	6	AX224395	Sequence
7	30	100.0	3343	15	AF360356	Zea mays
8	24.2	80.7	158	6	AX224396	Sequence
9	22	73.3	1304	6	AX523502	Sequence
10	21.6	72.0	185503	9	AC151282	Mus muscu
11	21.2	70.7	110000	15	AP008215	Continuation (212
12	21.2	70.7	110000	15	AP008208	Continuation (286
13	21.2	70.7	110000	15	AP008209	Continuation (322
14	21.2	70.7	110000	15	AP008212	Continuation (207
15	21.2	70.7	129778	15	AC091123	Continuation (207
16	21.2	70.7	140728	15	AP006548	Oryza sat
17	21.2	70.7	153675	14	AP005710	Oryza sat
18	21.2	70.7	155146	15	AP004118	Oryza sat

19	21.2	70.7	158374	15	AP004786	Oryza sat
20	21.2	70.7	172058	15	AP003682	Oryza sat
21	21.2	70.7	178158	15	AC084320	Oryza sat
22	21	70.0	89829	15	AC119671	Oryza sat
23	21	70.0	93342	8	AC087245	Homo sapi
24	21	70.0	110000	14	AC153053	Bos tauru
25	21	70.0	110000	15	AF008215	Continuation (76 o
26	21	70.0	110000	15	AF008216	Continuation (221
27	21	70.0	110000	15	AF008217	Continuation (75 o
28	21	70.0	110000	15	AF008217	Continuation (227
29	21	70.0	110000	15	AF008209	Continuation (287
30	21	70.0	123472	15	AC120984	Oryza sat
31	21	70.0	142015	15	AC120984	Oryza sat
32	21	70.0	143681	15	AC082645	Oryza sat
33	21	70.0	156394	14	AC082645	Oryza sat
34	21	70.0	158839	15	AC090882	Oryza sat
35	21	70.0	162198	15	AF005916	Oryza sat
36	21	70.0	187707	15	AC077693	Oryza sat
37	21	70.0	188854	9	AL626770	Mouse DNA
38	21	70.0	197160	15	AP005930	Oryza sat
39	21	70.0	253492	14	AC102160	Mus muscu
40	21	70.0	300029	15	AB017121	Oryza sat
41	21	70.0	345350	14	AC153038	Bos tauru
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43	20.6	68.7	169540	9	AC160062	Mus muscu
44	20.6	68.7	173088	15	AC109365	Oryza sat
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ALIGNMENTS

RESULT 1	AX224397	Sequence 4 from Patent WO0160997	30 bp	DNA	linear	PAT 10-SEP-2001
LOCUS	AX224397	AX224397.1	GI:15554639			
DEFINITION	AX224397	Sequence 4 from Patent WO0160997				
ACCESSION	AX224397	AX224397.1	GI:15554639			
VERSION	AX224397	AX224397.1	GI:15554639			
KEYWORDS	AX224397	AX224397.1	GI:15554639			
SOURCE	AX224397	AX224397.1	GI:15554639			
ORGANISM	AX224397	AX224397.1	GI:15554639			
REFERENCE	AX224397	AX224397.1	GI:15554639			
AUTHORS	AX224397	AX224397.1	GI:15554639			
TITLE	AX224397	AX224397.1	GI:15554639			
JOURNAL	AX224397	AX224397.1	GI:15554639			
FEATURES	AX224397	AX224397.1	GI:15554639			
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ORIGIN	AX224397	AX224397.1	GI:15554639			
Query Match	AX224397	AX224397.1	GI:15554639			
Best Local Similarity	AX224397	AX224397.1	GI:15554639			
Matches	AX224397	AX224397.1	GI:15554639			
Score	AX224397	AX224397.1	GI:15554639			
DB	AX224397	AX224397.1	GI:15554639			
QY	AX224397	AX224397.1	GI:15554639			
Db	AX224397	AX224397.1	GI:15554639			
RESULT 2	AX224402	Sequence 9 from Patent WO0160997	255 bp	DNA	linear	PAT 10-SEP-2001
LOCUS	AX224402	AX224402	GI:15554644			
DEFINITION	AX224402	AX224402	GI:15554644			
ACCESSION	AX224402	AX224402	GI:15554644			
VERSION	AX224402	AX224402	GI:15554644			
KEYWORDS	AX224402	AX224402	GI:15554644			
SOURCE	AX224402	AX224402	GI:15554644			

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ORGANISM      Zea mays
DEFINITION    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
ACCESSION     Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
VERSION       1
KEYWORDS      clade; Panicoideae; Andropogoneae; Zea.
ORGANISM      Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE         Male tissue-preferred regulatory region and method of using same
JOURNAL       Patent: WO 0160997-A 9 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES      Location/Qualifiers
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             /mol_type="unassigned DNA"
             /db_xref="taxon:4577"
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Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCACCGTTCGTCCTGTGTTCCA 30
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Db 39 CATGCTTGTTCACCGTTCGTCCTGTGTTCCA 68

RESULT 3
LOCUS          BD062176                1394 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION    Male tissue-preferred regulatory region and method of using same.
ACCESSION     BD062176
VERSION       BD062176.1 GI:22607781
KEYWORDS      JP 2001520523-A/1.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominoidea; Homo.
              1 (bases 1 to 1394)
              Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G.A. and
              Kendall,T.L.
              Male tissue-preferred regulatory region and method of using same
              Patent: JP 2001520523-A 1 30-OCT-2001;
              PIONEER HI-BRED INTERNATIONAL INC
              PN JP 2001520523-A/1
              PD 30-OCT-2001
              PF 19-JUN-1998 JP 1999504910
              PR 23-JUN-1997 US 08/880499
              PI MARC C ALBERTSEN,TIMOTHY W FOX,CARL W GARNAAT,GARY A HUFFMAN,
              TIMMY L KENDALL
              PC C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC
              ,C07K14/34,C12Q1/68,
              PC A01H5/00
              CC Strandedness: Single;
              CC Topology: Linear;
              FH Key Location/Qualifiers
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             1..1394
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCACCGTTCGTCCTGTGTTCCA 30
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Db 1179 CATGCTTGTTCACCGTTCGTCCTGTGTTCCA 1208

RESULT 5
LOCUS          AX224394                1394 bp      DNA      linear      PAT 10-SEP-2001
DEFINITION    Sequence 1 from Patent WO0160997.
ACCESSION     AX224394
VERSION       AX224394.1 GI:15554636
KEYWORDS      Zea mays
SOURCE        Zea mays
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
              1
              Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
              Male tissue-preferred regulatory region and method of using same
              Patent: WO 0160997-A 1 23-AUG-2001;
              PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES      Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1179 CATGCTTGTTCACCGTTCGTCCTGTGTTCCA 1208

RESULT 4
LOCUS          BD062177                1394 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION    Male tissue-preferred regulatory region and method of using same.
ACCESSION     BD062177
VERSION       BD062177.1 GI:22607782
KEYWORDS      JP 2001520523-A/2.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominoidea; Homo.
              1 (bases 1 to 1394)
              Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G.A. and
              Kendall,T.L.
              Male tissue-preferred regulatory region and method of using same
              Patent: JP 2001520523-A 2 30-OCT-2001;
              PIONEER HI-BRED INTERNATIONAL INC
              PN JP 2001520523-A/2
              PD 30-OCT-2001
              PF 19-JUN-1998 JP 1999504910
              PR 23-JUN-1997 US 08/880499
              PI MARC C ALBERTSEN,TIMOTHY W FOX,CARL W GARNAAT,GARY A HUFFMAN,
              TIMMY L KENDALL
              PC C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC
              ,C07K14/34,C12Q1/68,
              PC A01H5/00
              CC Strandedness: Single;
              CC Topology: Linear;
              FH Key Location/Qualifiers
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             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
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Query Match      100.0%; Score 30; DB 6; Length 1394;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Diadexus, Inc. (US)
 Location/Qualifiers
 1. .1304
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

FEATURES
 source

ORIGIN

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 Best Local Similarity 83.3%; Pred. No. 89;
 Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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 Db 1155 CTTCTGTGTCCTCTCTCTGTTCCA 1126
 |||||

RESULT 10
 AC151282/c
 LOCUS
 DEFINITION Mus musculus BAC clone RP23-461H1 from chromosome 17, complete sequence.

ACCESSION AC151282 AC124638
 VERSION AC151282.3 GI:71533339
 KEYWORDS HTG.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Tomlinson, C. and Cotton, M.
 TITLE The sequence of Mus musculus BAC clone RP23-461H1
 JOURNAL Unpublished (2001)
 REFERENCE 2 (bases 1 to 185503)
 AUTHORS Wilson, R.K.
 TITLE Direct Submission
 JOURNAL Submitted (24-AUG-2004) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 3 (bases 1 to 185503)
 AUTHORS Wilson, R.K.
 TITLE Direct Submission
 JOURNAL Submitted (12-JAN-2005) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 4 (bases 1 to 185503)
 AUTHORS Wilson, R.K.
 TITLE Direct Submission
 JOURNAL Submitted (30-JUL-2005) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT
 On Jul 30, 2005 this sequence version replaced gi:57544825.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu
 Contact: submissions@watson.wustl.edu
 ----- Summary Statistics
 Center project name: M_BA0461H01
 Drafting center: WIBR

NOTICE:
 This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e. phred quality >=30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone, fosmid clone or direct clone walk sequence. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to obtain the consensus sequence. The assembly was confirmed by restriction digest.
 This finishing standard has slightly changed from the previous Human standard. Specifically, standards for regions of low sequence

complexity (such as dinucleotide repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the mouse genome, and the return on extended finishing efforts is minimal.
 If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous bases, then the region is duly annotated.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu

SOURCE INFORMATION:
 The BAC Library has been constructed by Kazutoyo Oseegawa and Minako Tatenoe in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org

This sequence is the entire insert of the clone.

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 /db_xref="taxon:10090"
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 37190. .37291
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 37612. .37642
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 38054. .38103
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 38247. .38458
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 38459. .38760
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 40341. .40404
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 42926. .43056
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 95577. .95635
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 99723. .100104
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 151397. .151697
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ORIGIN
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 Best Local Similarity 85.7%; Pred. No. 1.4e+02;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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 Db 47380 ATGCTGTTCACACAGTTGATCTTGTTC 47353
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AP008215_008	800001	910000
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AP008215_167 16700001 16810000
AP008215_168 16800001 16910000
AP008215_169 16900001 17010000
AP008215_170 17000001 17110000
AP008215_171 17100001 17210000
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AP008215_190 19000001 19110000
AP008215_191 19100001 19210000
AP008215_192 19200001 19310000
AP008215_193 19300001 19410000
AP008215_194 19400001 19510000
AP008215_195 19500001 19610000
AP008215_196 19600001 19710000

Query Match 70.7%; Score 21.2; DB 15; Length 110000;
Best Local Similarity 88.5%; Fred. NO. 2.1e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CTGTGTTCAACCGTTCGTGTTGTTCA 30
Db 84254 CATGTTTAACCGTTCGTGTTTATTC 84279

RESULT 12
AP008208_285
WPCOMMENT
Sequence split into 360 fragments LOCUS AP008208 Accession AP008208
Fragment Name Begin End
AP008208_000 1 110000
AP008208_001 100001 210000
AP008208_002 200001 310000
AP008208_003 300001 410000
AP008208_004 400001 510000
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AP008208_005 500001 610000
AP008208_006 600001 710000
AP008208_007 700001 810000
AP008208_008 800001 910000
AP008208_009 900001 1010000
AP008208_010 1000001 1110000
AP008208_011 1100001 1210000
AP008208_012 1200001 1310000
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AP008208_014 1400001 1510000
AP008208_015 1500001 1610000
AP008208_016 1600001 1710000
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AP008208_018 1800001 1910000
AP008208_019 1900001 2010000
AP008208_020 2000001 2110000
AP008208_021 2100001 2210000
AP008208_022 2200001 2310000
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AP008208_077 7700001 7810000
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AP008208_078 7800001 7910000
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AP008208_081 8100001 8210000
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AP008208_083 8300001 8410000
AP008208_084 8400001 8510000
AP008208_085 8500001 8610000
AP008208_086 8600001 8710000
AP008208_087 8700001 8810000
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AP008208_191 19100001 19210000
AP008208_192 19200001 19310000
AP008208_193 19300001 19410000
AP008208_194 19400001 19510000
AP008208_195 19500001 19610000
AP008208_196 19600001 19710000

Query Match 70.7%; Score 21.2; DB 15; Length 110000;
Best Local Similarity 88.5%; Pred. No. 2.1e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 5 CTGTTCAACCGTTCGTCGTTGTTCCA 30
Db 29637 CATGTTTAAACCGTTCGTCGTTATTTCA 29662

RESULT 13
AP008209_322/c
WPCOMMENT
Sequence split into 362 fragments LOCUS AP008209 Accession AP008209
Fragment Name Begin End
AP008209_000 1 110000
AP008209_001 100001 210000
AP008209_002 200001 310000
AP008209_003 300001 410000
AP008209_004 400001 510000
AP008209_005 500001 610000
AP008209_006 600001 710000
AP008209_007 700001 810000
AP008209_008 800001 910000
AP008209_009 900001 1010000
AP008209_010 1000001 1110000
AP008209_011 1100001 1210000

AP008209_012	1200001	1310000	AP008209_085	8500001	8610000
AP008209_013	1300001	1410000	AP008209_086	8600001	8710000
AP008209_014	1400001	1510000	AP008209_087	8700001	8810000
AP008209_015	1500001	1610000	AP008209_088	8800001	8910000
AP008209_016	1600001	1710000	AP008209_089	8900001	9010000
AP008209_017	1700001	1810000	AP008209_090	9000001	9110000
AP008209_018	1800001	1910000	AP008209_091	9100001	9210000
AP008209_019	1900001	2010000	AP008209_092	9200001	9310000
AP008209_020	2000001	2110000	AP008209_093	9300001	9410000
AP008209_021	2100001	2210000	AP008209_094	9400001	9510000
AP008209_022	2200001	2310000	AP008209_095	9500001	9610000
AP008209_023	2300001	2410000	AP008209_096	9600001	9710000
AP008209_024	2400001	2510000	AP008209_097	9700001	9810000
AP008209_025	2500001	2610000	AP008209_098	9800001	9910000
AP008209_026	2600001	2710000	AP008209_099	9900001	10010000
AP008209_027	2700001	2810000	AP008209_100	1000001	10110000
AP008209_028	2800001	2910000	AP008209_101	10100001	10210000
AP008209_029	2900001	3010000	AP008209_102	10200001	10310000
AP008209_030	3000001	3110000	AP008209_103	10300001	10410000
AP008209_031	3100001	3210000	AP008209_104	10400001	10510000
AP008209_032	3200001	3310000	AP008209_105	10500001	10610000
AP008209_033	3300001	3410000	AP008209_106	10600001	10710000
AP008209_034	3400001	3510000	AP008209_107	10700001	10810000
AP008209_035	3500001	3610000	AP008209_108	10800001	10910000
AP008209_036	3600001	3710000	AP008209_109	10900001	11010000
AP008209_037	3700001	3810000	AP008209_110	11000001	11110000
AP008209_038	3800001	3910000	AP008209_111	11100001	11210000
AP008209_039	3900001	4010000	AP008209_112	11200001	11310000
AP008209_040	4000001	4110000	AP008209_113	11300001	11410000
AP008209_041	4100001	4210000	AP008209_114	11400001	11510000
AP008209_042	4200001	4310000	AP008209_115	11500001	11610000
AP008209_043	4300001	4410000	AP008209_116	11600001	11710000
AP008209_044	4400001	4510000	AP008209_117	11700001	11810000
AP008209_045	4500001	4610000	AP008209_118	11800001	11910000
AP008209_046	4600001	4710000	AP008209_119	11900001	12010000
AP008209_047	4700001	4810000	AP008209_120	12000001	12110000
AP008209_048	4800001	4910000	AP008209_121	12100001	12210000
AP008209_049	4900001	5010000	AP008209_122	12200001	12310000
AP008209_050	5000001	5110000	AP008209_123	12300001	12410000
AP008209_051	5100001	5210000	AP008209_124	12400001	12510000
AP008209_052	5200001	5310000	AP008209_125	12500001	12610000
AP008209_053	5300001	5410000	AP008209_126	12600001	12710000
AP008209_054	5400001	5510000	AP008209_127	12700001	12810000
AP008209_055	5500001	5610000	AP008209_128	12800001	12910000
AP008209_056	5600001	5710000	AP008209_129	12900001	13010000
AP008209_057	5700001	5810000	AP008209_130	13000001	13110000
AP008209_058	5800001	5910000	AP008209_131	13100001	13210000
AP008209_059	5900001	6010000	AP008209_132	13200001	13310000
AP008209_060	6000001	6110000	AP008209_133	13300001	13410000
AP008209_061	6100001	6210000	AP008209_134	13400001	13510000
AP008209_062	6200001	6310000	AP008209_135	13500001	13610000
AP008209_063	6300001	6410000	AP008209_136	13600001	13710000
AP008209_064	6400001	6510000	AP008209_137	13700001	13810000
AP008209_065	6500001	6610000	AP008209_138	13800001	13910000
AP008209_066	6600001	6710000	AP008209_139	13900001	14010000
AP008209_067	6700001	6810000	AP008209_140	14000001	14110000
AP008209_068	6800001	6910000	AP008209_141	14100001	14210000
AP008209_069	6900001	7010000	AP008209_142	14200001	14310000
AP008209_070	7000001	7110000	AP008209_143	14300001	14410000
AP008209_071	7100001	7210000	AP008209_144	14400001	14510000
AP008209_072	7200001	7310000	AP008209_145	14500001	14610000
AP008209_073	7300001	7410000	AP008209_146	14600001	14710000
AP008209_074	7400001	7510000	AP008209_147	14700001	14810000
AP008209_075	7500001	7610000	AP008209_148	14800001	14910000
AP008209_076	7600001	7710000	AP008209_149	14900001	15010000
AP008209_077	7700001	7810000	AP008209_150	15000001	15110000
AP008209_078	7800001	7910000	AP008209_151	15100001	15210000
AP008209_079	7900001	8010000	AP008209_152	15200001	15310000
AP008209_080	8000001	8110000	AP008209_153	15300001	15410000
AP008209_081	8100001	8210000	AP008209_154	15400001	15510000
AP008209_082	8200001	8310000	AP008209_155	15500001	15610000
AP008209_083	8300001	8410000	AP008209_156	15600001	15710000
AP008209_084	8400001	8510000	AP008209_157	15700001	15810000

AP008209_158	15900001	15910000	AP008212_019	19000001	2010000
AP008209_159	15900001	16010000	AP008212_020	2000001	2110000
AP008209_160	16000001	16110000	AP008212_021	2100001	2210000
AP008209_161	16100001	16210000	AP008212_022	2200001	2310000
AP008209_162	16200001	16310000	AP008212_023	2300001	2410000
AP008209_163	16300001	16410000	AP008212_024	2400001	2510000
AP008209_164	16400001	16510000	AP008212_025	2500001	2610000
AP008209_165	16500001	16610000	AP008212_026	2600001	2710000
AP008209_166	16600001	16710000	AP008212_027	2700001	2810000
AP008209_167	16700001	16810000	AP008212_028	2800001	2910000
AP008209_168	16800001	16910000	AP008212_029	2900001	3010000
AP008209_169	16900001	17010000	AP008212_030	3000001	3110000
AP008209_170	17000001	17110000	AP008212_031	3100001	3210000
AP008209_171	17100001	17210000	AP008212_032	3200001	3310000
AP008209_172	17200001	17310000	AP008212_033	3300001	3410000
AP008209_173	17300001	17410000	AP008212_034	3400001	3510000
AP008209_174	17400001	17510000	AP008212_035	3500001	3610000
AP008209_175	17500001	17610000	AP008212_036	3600001	3710000
AP008209_176	17600001	17710000	AP008212_037	3700001	3810000
AP008209_177	17700001	17810000	AP008212_038	3800001	3910000
AP008209_178	17800001	17910000	AP008212_039	3900001	4010000
AP008209_179	17900001	18010000	AP008212_040	4000001	4110000
AP008209_180	18000001	18110000	AP008212_041	4100001	4210000
AP008209_181	18100001	18210000	AP008212_042	4200001	4310000
AP008209_182	18200001	18310000	AP008212_043	4300001	4410000
AP008209_183	18300001	18410000	AP008212_044	4400001	4510000
AP008209_184	18400001	18510000	AP008212_045	4500001	4610000
AP008209_185	18500001	18610000	AP008212_046	4600001	4710000
AP008209_186	18600001	18710000	AP008212_047	4700001	4810000
AP008209_187	18700001	18810000	AP008212_048	4800001	4910000
AP008209_188	18800001	18910000	AP008212_049	4900001	5010000
AP008209_189	18900001	19010000	AP008212_050	5000001	5110000
AP008209_190	19000001	19110000	AP008212_051	5100001	5210000
AP008209_191	19100001	19210000	AP008212_052	5200001	5310000
AP008209_192	19200001	19310000	AP008212_053	5300001	5410000
AP008209_193	19300001	19410000	AP008212_054	5400001	5510000
AP008209_194	19400001	19510000	AP008212_055	5500001	5610000
AP008209_195	19500001	19610000	AP008212_056	5600001	5710000
AP008209_196	19600001	19710000	AP008212_057	5700001	5810000
			AP008212_058	5800001	5910000
			AP008212_059	5900001	6010000
			AP008212_060	6000001	6110000
			AP008212_061	6100001	6210000
			AP008212_062	6200001	6310000
			AP008212_063	6300001	6410000
			AP008212_064	6400001	6510000
			AP008212_065	6500001	6610000
			AP008212_066	6600001	6710000
			AP008212_067	6700001	6810000
			AP008212_068	6800001	6910000
			AP008212_069	6900001	7010000
			AP008212_070	7000001	7110000
			AP008212_071	7100001	7210000
			AP008212_072	7200001	7310000
			AP008212_073	7300001	7410000
			AP008212_074	7400001	7510000
			AP008212_075	7500001	7610000
			AP008212_076	7600001	7710000
			AP008212_077	7700001	7810000
			AP008212_078	7800001	7910000
			AP008212_079	7900001	8010000
			AP008212_080	8000001	8110000
			AP008212_081	8100001	8210000
			AP008212_082	8200001	8310000
			AP008212_083	8300001	8410000
			AP008212_084	8400001	8510000
			AP008212_085	8500001	8610000
			AP008212_086	8600001	8710000
			AP008212_087	8700001	8810000
			AP008212_088	8800001	8910000
			AP008212_089	8900001	9010000
			AP008212_090	9000001	9110000
			AP008212_091	9100001	9210000

Query Match Best Local Similarity 70.7%; Score 21.2; DB 15; Length 110000;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTCTTCAACCGTTCGCTTGTTCCA 30
Db 59047 CATGTTTAAACCGTTCGCTTGTTCCA 59022

RESULT 14
AP008212_206/c
WPCOMMENT
Sequence split into 308 fragments LOCUS AP008212 Accession AP008212

Fragment Name	Begin	End
AP008212_000	1	110000
AP008212_001	100001	210000
AP008212_002	200001	310000
AP008212_003	300001	410000
AP008212_004	400001	510000
AP008212_005	500001	610000
AP008212_006	600001	710000
AP008212_007	700001	810000
AP008212_008	800001	910000
AP008212_009	900001	1010000
AP008212_010	1000001	1110000
AP008212_011	1100001	1210000
AP008212_012	1200001	1310000
AP008212_013	1300001	1410000
AP008212_014	1400001	1510000
AP008212_015	1500001	1610000
AP008212_016	1600001	1710000
AP008212_017	1700001	1810000
AP008212_018	1800001	1910000

AP008212_092 9200001 9310000
AP008212_093 9300001 9410000
AP008212_094 9400001 9510000
AP008212_095 9500001 9610000
AP008212_096 9600001 9710000
AP008212_097 9700001 9810000
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AP008212_165 1650001 16610000
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AP008212_184 1840001 18510000
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AP008212_186 1860001 18710000
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AP008212_190 1900001 19110000
AP008212_191 1910001 19210000
AP008212_192 1920001 19310000
AP008212_193 1930001 19410000
AP008212_194 1940001 19510000
AP008212_195 1950001 19610000
AP008212_196 1960001 19710000

Query Match 70.7%; Score 21.2; DB 15; Length 110000;
Best Local Similarity 88.5%; Pred. No. 2.1e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CTGTTCACCGTTCGTCCTGTTCCA 30
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Db 59888 CAGTTTACCGTTCGTCCTGTTCAA 59863
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RESULT 15

AC091123/c AC091123 129778 bp DNA linear PLN 09-AUG-2001
LOCUS Oryza sativa chromosome 3 BAC OSJNB0093E13 genomic sequence,
DEFINITION complete sequence.

ACCESSION AC091123.4 GI:14670090

VERSION HTG.

KEYWORDS Oryza sativa (japonica cultivar-group)

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 129778)

1 (bases 1 to 129778)

Buell, C.R., Yuan, Q., Ouyang, S., Moffat, K.S., Hill, J.N.,

Gansberger, K., Brenner, M., Burgess, S., Hance, M., Shvartabeyn, M.,

Tsitlin, T., Riggs, F., Hsiao, J., Zismann, V., Blunt, S., Pai, G.,

VanAken, S.E., Utterback, T.R., Feldblyum, T.V., Quackenbush, J.,

Salzberg, S.L., White, O. and Fraser, C.M.

Oryza sativa chromosome 3 BAC OSJNB0093E13 genomic sequence

Unpublished

2 (bases 1 to 129778)

Buell, R.

Direct Submission

Submitted (31-MAR-2001) The Institute for Genomic Research, 9712

Medical Center Dr, Rockville, MD 20850, USA

3 (bases 1 to 129778)

Buell, R.

Direct Submission

Submitted (11-JUL-2001) The Institute for Genomic Research, 9712

Medical Center Dr, Rockville, MD 20850, USA


```
/translation="MEDWVVLGGDGSVELHGDSDVGGSDTESGFVVQVRGAAD
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GICEENPDDEIFDDEEESDDEEDIGSDLETDSDEYIEESTDEESDYEEEDTDLDES
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SDDEEDSYDEEDIDDEEESDCDEEIDDEEHEEHGKNKYDAIDNESFGEESCMQSDA
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AMQAAARNQAAAMVRAADIDSVMQAAAGGLAAQDVEALSQCATGLRAMAAAPSPA
VGVDVSAANTAAAFPLDTLALQDGVVSLAVFYLLFGVYVLLLRICALN"
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/rpt_family="(GGA)n"
complement(20115..20185)
repeat_region
/rpt_family="AT_rich"
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/gene="OSJNBb0093E13.8"
/notes="predicted by fgenesh"
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/gene="OSJNBb0093E13.8"
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/gene="OSJNBb0093E13.8"
/codon_start=1
/product="hypothetical protein"

Query Match 70.7%; Score 21.2; DB 15; Length 129778;
Best Local Similarity 88.5%; Pred. No. 2.1e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTTGTTCAACCGTTCGTCTGTTCCA 30
Db 20209 CATGTTAACCGTTCGTCTGTTCAA 20184
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Search completed: March 5, 2006, 21:55:36
Job time : 135.048 secs

GenCore version 5.1.7
Copyright (C) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 17:08:23 ; Search time 19.9642 Seconds
(without alignments)
10014.946 Million cell updates/sec

Title: US-10-713-381-1_COPY_1179_1208

Perfect score: 30

Sequence: 1 catgctgttcaacgctgtctgttccca 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001as:*
- 5: Geneseq2001bs:*
- 6: Geneseq2002as:*
- 7: Geneseq2002bs:*
- 8: Geneseq2003as:*
- 9: Geneseq2003bs:*
- 10: Geneseq2003cs:*
- 11: Geneseq2003ds:*
- 12: Geneseq2004as:*
- 13: Geneseq2004bs:*
- 14: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	5	AAH76335
2	30	100.0	255	5	AAH76340
3	30	100.0	1394	2	AAH7408
4	30	100.0	1394	2	AAH7409
5	30	100.0	1394	5	AAH76332
6	30	100.0	1394	5	AAH76333
7	24.2	80.7	158	5	AAH76334
8	22	73.3	1304	6	AEQ75351
9	20.4	68.0	1542	6	AEQ75351
10	20.2	67.3	2397	8	ABZ13819
11	20	66.7	2000	11	ACN44013
12	20	66.7	2000	11	ACN44013
13	20	66.7	2000	11	ACN44013
14	19.6	65.3	1735	12	ADJ40785
15	19.6	65.3	2000	8	ADJ40785
16	19.6	65.3	2000	8	ADJ40785
17	19.6	65.3	2000	8	ADJ40785
18	19.6	65.3	2000	8	ADJ40785
19	19.6	65.3	2000	11	ACN44013

C	20	19.6	65.3	2000	12	ADJ40977
	21	19.4	64.7	2240	2	AAQ47668
	22	19.4	64.7	2243	4	AAQ47668
	23	19.4	64.7	2243	9	AAQ47668
	24	19.4	64.7	349580	6	ABQ81845
	25	19.4	64.0	2000	8	ADJ40785
	26	19.2	63.3	1324	8	ADJ40785
	27	19	63.3	1388	3	AAQ47668
	28	19	63.3	1821	10	ADJ40785
	29	19	63.3	2000	11	ACN44013
	30	19	63.3	5671	4	AAQ47668
	31	19	63.3	5671	5	AAQ47668
	32	19	63.3	5671	5	AAQ47668
	33	19	63.3	5671	9	ADJ40785
	34	19	63.3	198522	11	ACN44013
	35	18.8	62.7	883	6	ABK65288
	36	18.8	62.7	883	10	ADJ40785
	37	18.8	62.7	883	10	ADJ40785
	38	18.8	62.7	883	12	ADJ40785
	39	18.8	62.7	1083	4	AAQ47668
	40	18.8	62.7	1083	8	AAQ47668
	41	18.8	62.7	1899	10	ADJ40785
	42	18.8	62.7	1902	4	AAQ47668
	43	18.8	62.7	1902	8	AAQ47668
	44	18.8	62.7	1908	12	ADJ40785
	45	18.8	62.7	2000	11	ACN44013

ALIGNMENTS

RESULT 1

AAH76335

ID AAH76335 standard; DNA; 30 BP.

AC AAH76335;

DT 29-OCT-2001 (first entry)

DE Z. mays Ms45 male tissue-preferred regulatory region fragment.

MS45; male tissue; regulatory region; transcription; male fertility;

KW hybrid seed; ds.

OS Zea mays.

PN WO200160997-A2.

PD 23-AUG-2001.

PF 13-FEB-2001; 2001WO-US004527.

PR 15-FEB-2000; 2000US-00504487.

PA (PION-) PIONEER HI-BRED INT INC.

PI Albertsen MC, Fox TW, Garnaat CW, Huifman G, Kendall TL;

DR WPI; 2001-514772/56.

PT A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.

PS Claim 5; Page 47; 50pp; English.

CC The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (i) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The

```
CC present sequence represents a DNA fragment -152 to -181 bases upstream of
CC the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region
CC nucleotide sequence
XX
SQ Sequence 30 BP; 4 A; 9 C; 5 G; 12 T; 0 U; 0 Other;

Query Match      100.0%; Score 30; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCACACCGTTCGTCCTGTGTTCCA 30
   |||||
Db 1 CATGCTTGTTCACACCGTTCGTCCTGTGTTCCA 30

RESULT 2
AAH76340
ID AAH76340 standard; DNA; 255 BP.
XX
AC AAH76340;
XX
DT 29-OCT-2001 (first entry)
XX
DE Z. mays Ms45 promoter fragment.
XX
KW Ms45; male tissue; regulatory region; transcription; male fertility;
KW hybrid seed; promoter; ds.
XX
OS Zea mays.
XX
PN WO200160997-A2.
XX
PD 23-AUG-2001.
XX
PF 13-FEB-2001; 2001WO-US004527.
XX
PR 15-FEB-2000; 2000US-00504487.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
XX
DR WPI; 2001-514772/56.
XX
CC A male tissue-preferred regulatory region comprising nucleotide sequences
CC essential for initiating transcription of the MS45 gene useful for
CC mediating fertility in a male plant.
XX
PS Example 5; Fig 8; 50pp; English.
XX
CC The invention provides a male tissue-preferred regulatory region (I)
CC comprising nucleotide sequences essential for initiating transcription of
CC the MS45 gene. A method of mediating male fertility in a plant is
CC provided that involves introducing an expression vector comprising a
CC promoter operably linked to (I) into a plant where the exogenous gene
CC impacts male fertility of the plant and (I) controls expression of the
CC exogenous gene. A method of producing hybrid seeds is also provided. The
CC present sequence represents a Z. mays Ms45 promoter fragment
XX
SQ Sequence 255 BP; 59 A; 86 C; 39 G; 71 T; 0 U; 0 Other;

Query Match      100.0%; Score 30; DB 5; Length 255;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCACACCGTTCGTCCTGTGTTCCA 30
   |||||
Db 39 CATGCTTGTTCACACCGTTCGTCCTGTGTTCCA 68

RESULT 3
AAH07408
ID AAH07408 standard; DNA; 1394 BP.
```

```
XX
AC AAH07408;
XX
DT 08-JUN-1999 (first entry)
XX
DE Zea mays Ms45 male tissue-preferred regulatory region.
XX
KW Ms45; male; tissue-preferred; regulatory region; plant cells;
KW plant tissue; differentiated; maize; hybrid seed; fertility; ss.
XX
XX Zea mays.
XX
PN WO9859061-A1.
XX
PD 30-DEC-1998.
XX
PF 19-JUN-1998; 98WO-US012895.
XX
PR 23-JUN-1997; 97US-00880499.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Albertsen MC, Fox TW, Garnaat CW, Huffman GA, Kendall TL;
XX
DR WPI; 1999-105628/09.
XX
CC New nucleic acid encoding a Ms45 male tissue-preferred regulatory region
CC - useful in mediating plant fertility, especially hybrid seed production.
XX
PS Claim 2; Page 22-23; 39pp; English.
XX
CC The sequence is that encoding an Ms45 male tissue-preferred regulatory
CC region. It may be used in the construction of a vector for a method of
CC producing exogenous genes in a male tissue- preferred manner, which is
CC useful in restoring or conferring fertility, such as in hybrid seed
CC production. In conferring fertility, a monocot/dicot plant is transformed
CC with the exogenous nucleotide sequence (a male sterility gene, preferably
CC Ms45), which encodes a product selected from auxins, rolB and dietheria
CC toxin. Hybrid seeds are produced by cross-pollinating maize male fertile
CC and infertile plants
XX
SQ Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;

Query Match      100.0%; Score 30; DB 2; Length 1394;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCACACCGTTCGTCCTGTGTTCCA 30
   |||||
Db 1179 CATGCTTGTTCACACCGTTCGTCCTGTGTTCCA 1208

RESULT 4
AAH07409
ID AAH07409 standard; DNA; 1394 BP.
XX
AC AAH07409;
XX
DT 08-JUN-1999 (first entry)
XX
DE Zea mays Ms45 male tissue-preferred regulatory region.
XX
KW Ms45; male; tissue-preferred; regulatory region; plant cells;
KW plant tissue; differentiated; hybrid seed; fertility; ss.
XX
XX Zea mays.
XX
PN WO9859061-A1.
XX
PD 30-DEC-1998.
XX
PR 19-JUN-1998; 98WO-US012895.
XX
```

PR 23-JUN-1997; 97US-00880499.
 PA (PION-) PIONEER HI-BRED INT INC.
 XX Albertsen MC, Fox TW, Garnaat CW, Huffman GA, Kendall TL;
 XX WPI; 1999-105628/09.
 XX
 XX New nucleic acid encoding a Ms45 male tissue-preferred regulatory region
 PT - useful in mediating plant fertility, especially hybrid seed production.
 XX
 XX Claim 3; Page 23-24; 39pp; English.
 XX
 XX The sequence is that encoding an Ms45 male tissue-preferred regulatory
 CC region. It may be used in the construction of a vector for a method of
 CC producing exogenous genes in a male tissue-preferred manner, which is
 CC useful in restoring or conferring fertility, such as in hybrid seed
 CC production. In conferring fertility, a monocot/dicot plant is transformed
 CC with the exogenous nucleotide sequence (a male sterility gene, preferably
 CC Ms45), which encodes a product selected from auxins, roib and diptheria
 CC toxin. Hybrid seeds are produced by cross-pollinating maize male fertile
 CC and infertile plants
 XX
 XX Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 30; DB 2; Length 1394;
 Best Local Similarity 100.0%; Pred. No. 0.007;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CATGCTTGTTCAACCGTTCGTTGTTCCA 30
 Db 1179 CATGCTTGTTCAACCGTTCGTTGTTCCA 1208
 RESULT 5
 AAH76332
 ID AAH76332 standard; DNA; 1394 BP.
 AC AAH76332;
 XX
 XX 29-OCT-2001 (first entry)
 XX
 XX Z. mays Ms45 male tissue-preferred regulatory region encoding DNA.
 XX Ms45; male tissue; regulatory region; transcription; male fertility;
 XX hybrid seed; ds.
 XX Zea mays.
 XX WO200160997-A2.
 XX 23-AUG-2001.
 XX 13-FEB-2001; 2001WO-US004527.
 XX 15-FEB-2000; 2000US-00504487.
 XX (PION-) PIONEER HI-BRED INT INC.
 XX Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
 XX WPI; 2001-514772/56.
 XX A male tissue-preferred regulatory region comprising nucleotide sequences
 PT essential for initiating transcription of the Ms45 gene useful for
 PT mediating fertility in a male plant.
 XX
 XX Claim 4; Page 46; 50pp; English.
 XX
 XX The invention provides a male tissue-preferred regulatory region (I)
 CC comprising nucleotide sequences essential for initiating transcription of
 CC the Ms45 gene. A method of mediating male fertility in a plant is
 CC provided that involves introducing an expression vector comprising a
 CC promoter operably linked to (I) into a plant where the exogenous gene
 CC impacts male fertility of the plant and (I) controls expression of the
 CC exogenous gene. A method of producing hybrid seeds is also provided. The
 CC present sequence represents a nucleic acid sequence encoding an Ms45 male
 CC -tissue preferred regulatory region from Z. mays
 XX
 XX Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 30; DB 2; Length 1394;
 Best Local Similarity 100.0%; Pred. No. 0.007;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CATGCTTGTTCAACCGTTCGTTGTTCCA 30
 Db 1179 CATGCTTGTTCAACCGTTCGTTGTTCCA 1208

CC promoter operably linked to (I) into a plant where the exogenous gene
 CC impacts male fertility of the plant and (I) controls expression of the
 CC exogenous gene. A method of producing hybrid seeds is also provided. The
 CC present sequence represents a nucleic acid sequence encoding an Ms45 male
 CC -tissue preferred regulatory region from Z. mays
 XX
 XX Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 30; DB 5; Length 1394;
 Best Local Similarity 100.0%; Pred. No. 0.007;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CATGCTTGTTCAACCGTTCGTTGTTCCA 30
 Db 1179 CATGCTTGTTCAACCGTTCGTTGTTCCA 1208
 RESULT 6
 AAH76333
 ID AAH76333 standard; DNA; 1394 BP.
 XX
 XX AAH76333;
 XX
 XX 29-OCT-2001 (first entry)
 XX
 XX Z. mays Ms45 male tissue-preferred regulatory region encoding DNA.
 XX Ms45; male tissue; regulatory region; transcription; male fertility;
 XX hybrid seed; ds.
 XX Zea mays.
 XX WO200160997-A2.
 XX 23-AUG-2001.
 XX 13-FEB-2001; 2001WO-US004527.
 XX 15-FEB-2000; 2000US-00504487.
 XX (PION-) PIONEER HI-BRED INT INC.
 XX Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
 XX WPI; 2001-514772/56.
 XX A male tissue-preferred regulatory region comprising nucleotide sequences
 PT essential for initiating transcription of the Ms45 gene useful for
 PT mediating fertility in a male plant.
 XX
 XX Claim 4; Page 47; 50pp; English.
 XX
 XX The invention provides a male tissue-preferred regulatory region (I)
 CC comprising nucleotide sequences essential for initiating transcription of
 CC the Ms45 gene. A method of mediating male fertility in a plant is
 CC provided that involves introducing an expression vector comprising a
 CC promoter operably linked to (I) into a plant where the exogenous gene
 CC impacts male fertility of the plant and (I) controls expression of the
 CC exogenous gene. A method of producing hybrid seeds is also provided. The
 CC present sequence represents a nucleic acid sequence encoding an Ms45 male
 CC -tissue preferred regulatory region from Z. mays
 XX
 XX Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 30; DB 5; Length 1394;
 Best Local Similarity 100.0%; Pred. No. 0.007;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CATGCTTGTTCAACCGTTCGTTGTTCCA 30
 Db 1179 CATGCTTGTTCAACCGTTCGTTGTTCCA 1208

PA (Scri) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 PI Harper JF, Kreps J, Wang X, Zhu T;
 XX WPI; 2002-304127/34.
 DR
 XX
 XX Identifying a stress condition to which a plant cell has been exposed and
 PT producing plants with increased tolerance to these abiotic stresses.
 XX
 XX
 PS Claim 144; SEQ ID NO 1624; 577pp + Sequence Listing; English.
 XX
 CC The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising: (a) contacting nucleic acid
 CC representative of expressed polynucleotides in the plant cell with an
 CC array or probes representative of the plant cell genome; and (b)
 CC detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
 CC in methods of the invention. Note: The sequence data for this patent is
 CC not represented in the printed specification but is based on sequence
 CC information supplied to Derwent by the European Patent Office.
 XX
 SQ Sequence 1542 BP; 345 A; 382 C; 370 G; 445 T; 0 U; 0 Other;
 Query Match 68.0%; Score 20.4; DB 6; Length 1542;
 Best Local Similarity 80.0%; Pred. No. 91;
 Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 1 CATGCTTTTCAACCGTTCGTTTCCA 30
 DB 237 CATGATGTTTCAACCAATCGTTCGTTTCCA 266
 RESULT 10
 ACA44013
 ID ACA44013 standard; DNA; 2397 BP.
 XX
 AC ACA44013;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Prokaryotic essential gene #25670.
 XX
 KW Antisense; ds; prokaryotic essential gene; cell proliferation;
 KW drug design; gene.
 OS Pseudomonas putida.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107;
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlson KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu RH;
 XX
 DR WPI; 2003-029926/02.
 DR P-PSDB; ABU04143.
 XX
 XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 14; SEQ ID NO 31883; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing of a gene in an operon required for
 CC proliferation or the activity of a polypeptide; (6) inhibiting cellular
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 2397 BP; 415 A; 825 C; 781 G; 376 T; 0 U; 0 Other;
 Query Match 67.3%; Score 20.2; DB 8; Length 2397;
 Best Local Similarity 86.0%; Pred. No. 1.2e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1 CATGCTTTTCAACCGTTCGTTG 25
 DB 516 CATGCTGTATCAACCGTTCGCTTG 540
 RESULT 11
 ACL37526
 ID ACL37526 standard; cDNA; 2000 BP.
 XX
 AC ACL37526;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Rice stress-regulated promoter SEQ ID NO:16089.
 XX
 KW ss; abiotic stress tolerance; transgenic plant; plant; cereal;
 KW agriculture.
 XX
 OS Oryza sativa.
 XX
 PN WO2003008540-A2.
 XX
 PD 30-JAN-2003.
 XX
 PF 21-JUN-2002; 2002WO-US019668.
 XX
 PR 22-JUN-2001; 2001US-0300112P.
 PR 24-AUG-2001; 2001US-0314662P.
 PR 26-SEP-2001; 2001US-0325277P.
 PR 21-NOV-2001; 2001US-0332132P.
 XX

```

PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI Krepis J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Ricke D, Zhu T;
XX
XX WPI; 2003-248011/24.
XX
XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
XX Claim 48; SEQ ID NO 16089; 89pp; English.
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
SQ Sequence 2000 BP; 607 A; 443 C; 399 G; 549 T; 0 U; 2 Other;

Query Match 66.7%; Score 20; DB 11; Length 2000;
Best Local Similarity 82.1%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TGCTTGTTCACCGTTCGCTCTGTTCCTCA 30
Db 1576 TGCATGTTGACCGTTCGCTCTATTTCAA 1603

RESULT 12
ACL34976
ID ACL34976 standard; cDNA; 2000 BP.
XX
AC ACL34976;
XX
DT 02-JUN-2005 (first entry)
XX
DE Rice stress-regulated promoter SEQ ID NO:13539.
XX
KW ss; abiotic stress tolerance; transgenic plant; plant; cereal;
KW agriculture.
XX
OS Oryza sativa.
XX
PN WO2003008540-A2.
XX
PD 30-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019668.
XX
PR 22-JUN-2001; 2001US-0300112P.
PR 24-AUG-2001; 2001US-0314662P.
PR 26-SEP-2001; 2001US-0325277P.
PR 21-NOV-2001; 2001US-0332132P.
XX
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI Krepis J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Ricke D, Zhu T;
XX
XX WPI; 2003-248011/24.
XX
XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
XX Claim 48; SEQ ID NO 16089; 89pp; English.
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
SQ Sequence 2000 BP; 552 A; 438 C; 444 G; 566 T; 0 U; 0 Other;

Query Match 66.7%; Score 20; DB 11; Length 2000;
Best Local Similarity 82.1%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TGCTTGTTCACCGTTCGCTCTGTTCCTCA 30
Db 1179 TACATGTTTAAACCGTTCGCTCTATTTCAA 1206

RESULT 13
ADJ40785
ID ADJ40785 standard; cDNA; 2000 BP.
XX
AC ADJ40785;
XX
DT 06-MAY-2004 (first entry)
XX
DE Plant cDNA #1785.
XX
KW Plant; gene; ss; transcription; plant genome augmentation; cereal;
KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
KW antifungal.
XX
OS Eukaryota.
XX
PN US2004016025-A1.
XX
PD 22-JAN-2004.
XX
PF 26-SEP-2002; 2002US-00260238.
XX
PR 26-SEP-2001; 2001US-0325277P.
PR 26-SEP-2001; 2001US-0325448P.
PR 04-APR-2002; 2002US-0370620P.
XX
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KEP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
XX
PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;

```

PI Goff SA, Katagiri F, Kreps J, Provart N, Rieke D, Zhu T;
XX WPI; 2004-190374/18.
XX
XX New rice promoter, useful for manipulating crop plants to alter or
PT improve phenotypic characteristics e.g. produce large quantities of oil
PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
PT or high nutritional value.
XX
XX Claim 26; SEQ ID NO 1785; 230pp; English.
XX
XX The invention relates to plant nucleotide sequences that direct seed-,
CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
CC or constitutive transcription of an operatively linked nucleic acid
CC segment. The invention also relates to a method for augmenting a plant
CC genome and a method of identifying a gene, where its expression is
CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
CC proteins, to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 2000 BP; 552 A; 438 C; 444 G; 566 T; 0 U; 0 Other;
Query Match 66.7%; Score 20; DB 12; Length 2000;
Best Local Similarity 82.1%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 TCGTTGTCACCGTTCGTCTGTTCCTCA 30
DB 1179 TACATGTTTAAACCGTTCGTCTTATTCAA 1206
RESULT 14
ACL35519
ID ACL35519 standard; cDNA; 1735 BP.
XX
AC ACL35519;
XX
DT 02-JUN-2005 (first entry)
XX
DE Rice stress-regulated promoter SEQ ID NO:14082.
XX
KW as; abiotic stress tolerance, transgenic plant; plant; cereal;
XX agriculture.
XX
OS Oryza sativa.
XX
PN WO2003008540-A2.
XX
PD 30-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019668.
XX
PR 22-JUN-2001; 2001US-0300112P.
XX
PR 24-AUG-2001; 2001US-0314662P.
XX
PR 26-SEP-2001; 2001US-0325277P.
XX
PR 21-NOV-2001; 2001US-0332132P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Rieke D, Zhu T;
XX WPI; 2003-248011/24.

XX
PT New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
XX Claim 48; SEQ ID NO 14082; 89pp; English.
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
SQ Sequence 1735 BP; 502 A; 368 C; 279 G; 581 T; 0 U; 5 Other;
Query Match 65.3%; Score 19.6; DB 11; Length 1735;
Best Local Similarity 84.6%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5 CTGTTCACCGTTCGTCTGTTCCTCA 30
DB 394 CATGTTTAAACCGTTCGTCTTATTCAA 419
RESULT 15
ADAY2061
ID ADAY2061 standard; DNA; 2000 BP.
XX
AC ADAY2061;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 5386.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
XX gene; ds.
XX
OS Oryza sativa.
XX
PN WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX WPI; 2003-175290/17.
XX
XX Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
XX Claim 27; SEQ ID NO 5386; 89pp; English.
XX
XX The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in

CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.

xx
SQ Sequence 2000 BP; 605 A; 377 C; 326 G; 590 T; 0 U; 2 Other;

Query Match 65.3%; Score 19.6; DB 8; Length 2000;
Best Local Similarity 84.6%; Pred. No. 2.1e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 CTTGTTCAACCGTTGCTGTTGTTCCA 30
| ||||| ||||| ||||| |||||
Db 974 CATGTTTAACCGTTGCTGTTATTCAA 999

Search completed: March 5, 2006, 18:11:38
Job time : 22.9642 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 18:11:59 ; Search time 141.632 Seconds
(without alignments)
9910.279 Million cell updates/sec

Title: US-10-713-381-1_COPY_1179_1208

Sequence: 1 catgctgttcaaccgttgcgttgcctca 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*
10: gb_est10.*
11: gb_est11.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	30	100.0	687	9	CC656939	CG224225 OGDQ20TV
C 2	30	100.0	915	10	CC224225	CG224225 OGDQ20TV
C 3	30	100.0	963	9	CC656939	CG224225 OGDQ20TV
C 4	27.4	91.3	296	10	CG700474	CG700474 ZMBB001f1
C 5	22.2	74.0	534	5	BU035739	BU035739 QHJ7N19.Y
C 6	21.2	70.7	626	5	BU030489	BU030489 QHJ7N19.Y
C 7	21.2	70.7	792	7	CN137013	CN137013 OX1 54 E0
C 8	21.2	70.7	792	7	CN137013	CN137013 OX1 54 E0
C 9	21	70.0	154	1	AA811551	AA811551 oag9e03.s
C 10	21	70.0	351	11	CR192459	CR192459 Reverse s
C 11	21	70.0	571	11	CR064270	CR064270 Reverse s
C 12	21	70.0	599	11	CR233964	CR233964 Reverse s
C 13	21	70.0	769	11	CR188179	CR188179 Reverse s
C 14	21	70.0	835	9	CC848693	CC848693 NDL-2114
C 15	21	70.0	835	9	CC860012	CC860012 NDL-2114
C 16	20.8	69.3	586	7	CO853973	CO853973 LM SH5.00
C 17	20.6	68.7	412	8	R12648	R12648 yf57f08.r1
C 18	20.6	68.7	450	8	R12618	R12618 yf57f08.r1
C 19	20.6	68.7	582	1	AU290776	AU290776 AU290776
C 20	20.6	68.7	594	8	DR437963	DR437963 ACAC-aab6
C 21	20.6	68.7	681	9	AZ817790	AZ817790 ZM0087022
C 22	20.6	68.7	1144	9	CC271930	CC271930 CH261-112

23	20.4	68.0	353	9	AQ61553	AQ61553 CITBI-E1-
24	20.4	68.0	373	3	BP857382	BP857382 BP857382
25	20.4	68.0	396	2	BE522930	BE522930 M30D4STM
26	20.4	68.0	396	3	BP836596	BP836596 BP836596
27	20.4	68.0	514	2	BP354154	BP354154 00661 lea
28	20.4	68.0	515	3	BP561510	BP561510 BP561510
29	20.4	68.0	536	1	AV439701	AV439701 AV439701
30	20.4	68.0	559	1	AV825937	AV825937 AV825937
C 31	20.4	68.0	560	6	CA230882	CA230882 SCJFPL3C0
C 32	20.4	68.0	590	7	CV153842	CV153842 Euginetus
C 33	20.4	68.0	598	10	CW788317	CW788317 SP_Ba004
C 34	20.4	68.0	602	9	BH876120	BH876120 hr29B04.g
C 35	20.4	68.0	602	10	CL583422	CL583422 OB_Ba007
C 36	20.4	68.0	603	9	BZ694195	BZ694195 SP_Ba004
C 37	20.4	68.0	615	9	AQ453944	AQ453944 HS_5165.B
C 38	20.4	68.0	639	7	CV153844	CV153844 Euginetus
C 39	20.4	68.0	668	9	AQ260121	AQ260121 CITBI-E1
C 40	20.4	68.0	779	6	CD825116	CD825116 BN35.059M
C 41	20.4	68.0	807	6	CD836362	CD836362 BN45.0481
C 42	20.4	68.0	836	9	BH480110	BH480110 BOGRI44TR
C 43	20.4	68.0	967	9	BZ684538	BZ684538 PUBGQ31TD
C 44	20.4	68.0	1205	9	BI0570	BI0570 T15J6-T7 TA
C 45	20.2	67.3	431	8	R32995	R32995 YH73G09.r1

ALIGNMENTS

RESULT 1
LOCUS CC656939 687 bp DNA linear GSS 19-JUN-2003
DEFINITION OGDQ20TV ZM.0.7.1.5 KB Zea mays genomic clone ZMBMa0554D15,
genomic survey sequence.
ACCESSION CC656939
VERSION CC656939.1 GI:32060231
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade: Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 687)
AUTHORS Whitlaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Frazer,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGDQ20TV
Contact: Cathy Whitlaw
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitlaw@tigr.org
Seq primer: TF
Class: methylation filtered.
Location/Qualifiers
1. 687
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBMa0554D15"
/notes="lib=ZM.0.7.1.5 KB"
/clone-Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 100.0%; Score 30; DB 9; Length 687;
Best Local Similarity 100.0%; Pred. NO. 0.024;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGCTGTTCACCGCTTCGCTTGTTCCA 30

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Db      397 CATGCTTGTTCAACCGTTCGTCTGTGTTCCA 368
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RESULT 2
CG224225 OGIAG08TV_ZM_0.7_1.5_KB DNA linear GSS 22-AUG-2003
LOCUS     915 bp
DEFINITION OGIAG08TV_ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0716B15,
genomic survey sequence.
ACCESSION CG224225
VERSION    CG224225.1 GI:34124113
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 915)
AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
TITLE     Consortium for Maize Genomics
JOURNAL   Unpublished (2002)
COMMENT   Other_GSSs: OGIAG08TV
Contact: Cathy Whitelaw
TIGR      9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.
Location/Qualifiers
1. 915
/organism="Zea mays"
/mol_type="genomic DNA"
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/db_xref="taxon:4577"
/clone_lib="ZMMBMA0716B15"
/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

FEATURES
source
1. 915
Query Match 100.0%; Score 30; DB 10; Length 915;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGCTTGTTCAACCGTTCGTCTGTGTTCCA 30
|||||
Db      776 CATGCTTGTTCAACCGTTCGTCTGTGTTCCA 805
|||||

RESULT 4
CW445575
LOCUS     296 bp DNA linear GSS 02-NOV-2004
DEFINITION fbb001f170m16k0 Sorghum methylation filtered library (LibID: 104)
Sorghum bicolor genomic clone fbb001f170m16, genomic survey
sequence.
ACCESSION CW445575
VERSION    CW445575.1 GI:55193536
KEYWORDS   GSS.
SOURCE     Sorghum bicolor (sorghum)
ORGANISM   Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 296)
AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holeman,H., Roe,B.A., Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddelloh,J.A. and
Martinsen,R.A.
TITLE     Sorghum genome sequencing by methylation filtration
JOURNAL   PLOS Biol. 3 (1), e13 (2005)
PUBMED    15660154
COMMENT   Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: fbb001f170 row: m column: 16
Seq primer: k Reverse
Class: methylation filtered
High quality sequence stop: 296.
Location/Qualifiers
1. 296
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone_lib="fbb001f170m16"
/notes="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
prepared from purified nuclei was randomly sheared,

FEATURES
source
1. 296
/organism="Sorghum bicolor"
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/db_xref="taxon:4558"
/clone_lib="fbb001f170m16"
/notes="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
prepared from purified nuclei was randomly sheared,

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end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBSK(-) vector and electroporated into *E. coli* cells. This is a methylation filtered library."

ORIGIN

Query Match 91.3%; Score 27.4; DB 10; Length 296;
Best Local Similarity 96.6%; Pred. No. 0.3; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 ATGCTGTTCACCGTTCGTCCTTCTTCCA 30
|||||
Db 140 ATGCTGTTCACCGTTCGTCCTTCTTCCA 168

RESULT 5

CG700474/c
LOCUS ZMMBc0174H15f ZMMBc (EcoRI) Zea mays genomic clone ZMMBc0174H15
DEFINITION 308 bp DNA linear GSS 15-OCT-2003
5', genomic survey sequence.
ACCESSION CG700474
VERSION CG700474.1 GI:37688275
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 308)
Bharti A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,
Zohovetz, V., Fuks, G., Yu, R., Wing, R. and Messing, J.
Sequencing of the maize genome at PEIR (2003c)
Unpublished (2003)

TITLE

Sequencing of the maize genome at PEIR (2003c)

JOURNAL

Unpublished (2003)

COMMENT

Contact: Bharti, A.K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 57.

FEATURES

source

1..308
/organism="Zea mays"
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/cultivar="B73"
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/clone_lib="ZMMBc (EcoRI)"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN

Query Match 74.0%; Score 22.2; DB 10; Length 308;
Best Local Similarity 88.9%; Pred. No. 60;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATGCTGTTCACCGTTCGTCCTTCTT 27
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Db 226 CATGCTGTTCACCGTTCGTCCTTCTT 200
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RESULT 6

BU035739/c
LOCUS BU035739 534 bp mRNA linear EST 23-AUG-2002
DEFINITION QJ7N19.yg.ab1 QJ7N19 sunflower RHA280 Helianthus annuus cDNA
clone QJ7N19, mRNA sequence.
ACCESSION BU035739
VERSION BU035739.1 GI:22471259
KEYWORDS EST.

SOURCE

ORGANISM Helianthus annuus (common sunflower)

Helianthus annuus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.

REFERENCE

AUTHORS

Kozik A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
Ellison, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://comgenomics.ucdavis.edu/

TITLE

JOURNAL

COMMENT

Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Ammundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659

Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
belongs to contig QH_CA_Contig3046, see http://cgdb.ucdavis.edu/
for details.

Plate: QHJ7 row: N column: 19.

FEATURES

Location/Qualifiers

1..534
/organism="Helianthus annuus"
/mol_type="mRNA"
/cultivar="RHA280"
/db_xref="taxon:4232"
/clone="QHJ7N19"
/lab_host="E. coli"
/clone_lib="QH EFGHJ sunflower RHA280"
/note="Vector: pBSCDNASFIAB. The library was constructed
from 11 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_TISSUE=flowers environmental stress
TAG_LIB=QH EFGHJ sunflower RHA280
TAG_SEQ=CGAATGCGG3"

ORIGIN

Query Match 70.7%; Score 21.2; DB 5; Length 534;
Best Local Similarity 88.5%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGCTGTTCACCGTTCGTCCTTGT 27
|||||

Db 104 ATGCTGTTCACCGTTCGTCCTTGT 79
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RESULT 7

BU030489/c
LOCUS BU030489 626 bp mRNA linear EST 23-AUG-2002
DEFINITION QJ15120.yg.ab1 QJ15120 sunflower RHA280 Helianthus annuus cDNA
clone QJ15120, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Helianthus annuus (common sunflower)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.

REFERENCE

AUTHORS

Kozik A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,

Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
 Lai, Z., Church, S., Jackson, L. and Bradford, K.
 Lettuce and Sunflower ESTs from the Compositae Genome Project
<http://compenomics.ucdavis.edu/>
 Unpublished (2002)
 Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Amundson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@atgc.org [michelmore@vegmil.ucdavis.edu]
 belongs to contig QH_CA_Contig3046, see <http://cgpdb.ucdavis.edu/>
 for details.
 Plate: QHJ15 row: I column: 20.

FEATURES

source
 Location/Qualifiers
 1..626
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="RHA280"
 /db_xref="taxon:4232"
 /clone="QHJ15120"
 /lab_hosts="E.coli"
 /clone_lib="OH EFGHJ sunflower RHA280"
 /note="Vector: pRcDNASf1AB: The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cgpdb.ucdavis.edu/>
 TAG TISSUE=flowers environmental stress
 TAG LIB=OH EFGHJ sunflower RHA280
 TAG_SEQ=CGAATCGGG"

ORIGIN

Query Match 70.7%; Score 21.2; DB 5; Length 626;
 Best Local Similarity 88.5%; Pred. No. 1.9e+02;
 Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 ATGCTGTTCAACCGTTCGTCGTTCTT 27
 Db 104 ATGCTTCTTCAAGCGTTCGTCGTTT 79

RESULT 8
 LOCUS CN137013 792 bp mRNA linear EST 01-APR-2004
 DEFINITION OX1_54_E01.g1_A002 Oxidatively-stressed leaves and roots Sorghum bicolor cDNA Clone OX1_54_E01_A002 5', mRNA sequence.
 ACCESSION CN137013
 VERSION CN137013.1 GI:45970259
 KEYWORDS EST.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
 REFERENCE 1 (bases 1 to 792)
 AUTHORS Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.
 TITLE An EST database from Sorghum: oxidatively stressed leaves and roots Unpublished (2003)
 JOURNAL Other ESTs: OX1_54_E01.b1.A002
 COMMENT Contact: Cordonnier-Pratt, MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science, plant material and RNA prepared at Texas A & M University; sequencing done in the laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
 Seq primer: Sug5 (CTTCTGCTCTAAAGCTGGC).

FEATURES

source
 Location/Qualifiers
 1..792
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /cultivar="BTx623"
 /db_xref="taxon:4558"
 /clone="OX1_54_E01_A002"
 /lab_hosts="DH10B-TI phage-resistant E. coli"
 /clone_lib="Oxidatively-stressed leaves and roots"
 /note="Organ: Leaf and Root; Vector: pME185-FL3; Site 1: XhoI; Site 2: XhoI; The library was prepared from polyA+ RNA from oxidatively stressed, hydroponically grown sorghum seedlings. At 8 days of age, growth medium was supplemented with hydrogen peroxide to 0.003% and leaves were harvested at 3, 12 and 27 hr after treatment and all tissue pooled. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME185-FL3 vector (5-prime DraIII site is CACTGTGG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

ORIGIN

Query Match 70.7%; Score 21.2; DB 7; Length 792;
 Best Local Similarity 88.5%; Pred. No. 1.9e+02;
 Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 5 CTGTTCACCGTTCGTCGTTCTTCCA 30
 Db 17 CTCTCCACCGTTCGTCGTTCTTCCA 42

RESULT 9
 LOCUS AA811551/c 154 bp mRNA linear EST 19-FEB-1998
 DEFINITION Oa99a03.s1 NCI_CGAP GCB1 Homo sapiens cDNA clone IMAGE:1320412 3', similar to SW:COPE_BOVIN_Q28104 COATOMER EPSILON SUBUNIT ;, mRNA sequence.

ACCESSION AA811551.1 GI:2881162
 VERSION AA811551
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 154)
 AUTHORS NCI_CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsb@mail.nih.gov
 Tissue procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Trace considered overall poor quality

Insert Length: 1232 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .154

FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1320412"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI CGAP CB1"
/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTACCAATCTGAAGTGGAGCGCGCCCTCAATTTTTTTTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 70.0%; Score 21; DB 1; Length 154;
Best Local Similarity 82.8%; Pred. No. 1.8e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGCTGTTCACCGTTCGTCGTTCCTCA 30
DB 43 AAGCTGTTCACCGTTCGTCGTTCCTCA 15

RESULT 10

CR192459/c
LOCUS
DEFINITION Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN146a06, genomic survey sequence.
ACCESSION CR192459
VERSION CR192459.1 GI:49971308
KEYWORDS GSS; genome survey sequence; MICER.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 351)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.

TITLE Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, UK. http://www.sanger.ac.uk/MICER
FEATURES
source
Location/Qualifiers
1. .351

/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN146a06"
/clone_lib="MHPN"

ORIGIN

Query Match 70.0%; Score 21; DB 1; Length 351;
Best Local Similarity 82.8%; Pred. No. 2.1e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGCTGTTCACCGTTCGTCGTTCCTCA 30
DB 307 ATGCTGTTCACCGTTCGTCGTTCCTCA 279

RESULT 11

CR064270/c
LOCUS
DEFINITION Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN190119, genomic survey sequence.
ACCESSION CR064270
VERSION CR064270.1 GI:49797742
KEYWORDS GSS; genome survey sequence; MICER.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 571)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.

TITLE Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, UK. http://www.sanger.ac.uk/MICER
FEATURES
source
Location/Qualifiers
1. .571

/organism="Mus musculus"
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/clone_lib="MHPN"

ORIGIN

Query Match 70.0%; Score 21; DB 1; Length 571;
Best Local Similarity 82.8%; Pred. No. 2.2e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGCTGTTCACCGTTCGTCGTTCCTCA 30
DB 309 ATGCTGTTCACCGTTCGTCGTTCCTCA 281

RESULT 12

CR233964/c
LOCUS
DEFINITION Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN144h08, genomic survey sequence.
ACCESSION CR233964
VERSION CR233964.1 GI:50012813
KEYWORDS GSS; genome survey sequence; MICER.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 599)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.

TITLE Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, UK. http://www.sanger.ac.uk/MICER
FEATURES
source
Location/Qualifiers
1. .599

/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN144h08"
/clone_lib="MHPN"

ORIGIN

Query Match 70.0%; Score 21; DB 1; Length 599;
Best Local Similarity 82.8%; Pred. No. 2.3e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGCTGTTCACCGTTCGTCGTTCCTCA 30

Wed Mar 8 14:16:28 2006

us-10-713-381-1_copy_1179_1208.rst

Page 7

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 21:54:12 ; Search time 8.38752 Seconds
(without alignments)
6357.883 Million cell updates/sec

Title: US-10-713-381-1_COPY_1179_1208

Perfect score: 30

Sequence: 1.catgctgttcaaccgtctgttccca 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:**

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- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:**
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:**
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:**
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq:**
- 6: /cgn2_6/ptodata/1/ina/PCUS COMB.seq:**
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq:**
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:**
- 9: /cgn2_6/ptodata/1/ina/backfile1.seq:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	1394	3	US-08-880-499-1
2	30	100.0	1394	3	US-08-880-499-2
3	19.4	64.7	2243	2	US-07-937-609-15
4	19.4	64.7	2243	3	US-08-029-170-15
5	19.4	64.7	2243	3	US-09-443-745-15
6	19	63.3	45571	3	US-09-949-016-18262
7	18.8	62.7	7812	3	US-09-368-590-1
8	18.8	62.7	8756	3	US-09-949-016-1438
9	18.8	62.7	112874	3	US-08-961-527-132
10	18.8	62.7	112874	3	US-09-949-016-13180
11	18.6	62.0	549	3	US-09-270-767-29480
12	18.6	62.0	1120	3	US-09-270-767-13492
13	18.4	61.3	1260	3	US-09-248-796A-3293
14	18.2	60.7	2710	3	US-09-573-080A-7
15	18	60.0	601	3	US-09-949-016-200252
16	18	60.0	601	3	US-09-949-016-200253
17	18	60.0	889	3	US-08-956-171E-1190
18	18	60.0	889	3	US-08-781-986A-1190
19	18	60.0	1591	2	US-08-728-956-3
20	18	60.0	33675	3	US-09-921-992-2
21	18	60.0	111509	3	US-09-949-016-17379
22	18	60.0	254366	3	US-09-822-871-3
23	17.8	59.3	393	3	US-09-583-110-1388
24	17.8	59.3	393	3	US-09-107-433-743

ALIGNMENTS

RESULT 1
US-08-880-499-1
; Sequence 1, Application US/08880499
; Patent No. 6037523
; GENERAL INFORMATION:
; APPLICANT: Albertson, Marc C.
; APPLICANT: Fox, Tim W.
; APPLICANT: Hufman, Gary A.
; APPLICANT: Kendall, Timmy L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
; TITLE OF INVENTION: AND METHOD OF USING SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
; STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
; STREET: Box 1000
; CITY: Johnston
; STATE: Iowa
; COUNTRY: USA
; ZIP: 50131
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880.499
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sweeney, Patricia A.
; REGISTRATION NUMBER: 32,733
; REFERENCE/DOCKET NUMBER: 0578
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800
; TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1394 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-880-499-1

Query Match 100.0%; Score 30; DB 3; Length 1394;

Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCAACCGTTCGTCCTGTGTTCCA 30
Db 1179 CATGCTTGTTCAACCGTTCGTCCTGTGTTCCA 1208

RESULT 2

US-08-880-499-2
; Sequence 2, Application US/08880499
; Patent No. 6037523
; GENERAL INFORMATION:
; APPLICANT: Albertson, Marc C.
; APPLICANT: Fox, Tim W.
; APPLICANT: Carl, Garmaat W.
; APPLICANT: Huffman, Gary A.
; APPLICANT: Kendall, Timmy L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
; TITLE OF INVENTION: AND METHOD OF USING SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
; STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
; STREET: Box 1000
; CITY: Johnston
; STATE: Iowa
; COUNTRY: USA
; ZIP: 50131
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,499
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sweeney, Patricia A.
; REGISTRATION NUMBER: 32,733
; REFERENCE/DOCKET NUMBER: 0578
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800
; TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1394 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-880-499-2

Query Match 100.0%; Score 30; DB 3; Length 1394;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCAACCGTTCGTCCTGTGTTCCA 30
Db 1179 CATGCTTGTTCAACCGTTCGTCCTGTGTTCCA 1208

RESULT 3

US-07-937-609-15
; Sequence 15, Application US/07937609
; Patent No. 5319073
; GENERAL INFORMATION:
; APPLICANT: WANK, Stephen A.
; TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
; TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/937,609
FILING DATE: 19920902
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2243 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: rat brain CCKB receptor
FEATURE:
NAME/KEY: CDS
LOCATION: 136..1494
US-07-937-609-15

Query Match 64.7%; Score 19.4; DB 2; Length 2243;
Best Local Similarity 79.3%; Pred. No. 55;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCAACCGTTCGTCCTGTGTTCC 29
Db 5 CCTGCTTGCTCAACTCTACGCTGTGTTTC 33

RESULT 4

US-08-029-170-15
; Sequence 15, Application US/08029170
; Patent No. 6169173
; GENERAL INFORMATION:
; APPLICANT: WANK, Stephen A.
; TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
; TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/029,170
 FILING DATE: 19930310
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/937,609
 FILING DATE: 02-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/928,033
 FILING DATE: 11-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/861,769
 FILING DATE: 01-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/831,248
 FILING DATE: 07-FEB-1992

PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 40399/166 NIHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)836-9300

TELEFAX: (703)683-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 2243 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

IMMEDIATE SOURCE:

CLONE: rat brain CCKB receptor

FEATURE:

NAME/KEY: CDS

LOCATION: 136..1494

US-08-029-170-15

Query Match

Best Local Similarity 64.7%; Score 19.4; DB 3; Length 2243;

Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 CATGCTTGTTCAACCGTTCGTCCTGTTTC 29

Db 5 CCGCTTGCTCAACTCTACGCTTGTTTC 33

RESULT 5

US-09-443-745-15

Sequence 15, Application US/09443745

Patent No. 6706493

GENERAL INFORMATION:

APPLICANT: WANK, Stephen A.

TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/443,745

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION NUMBER: 08/029,170

FILING DATE: 10-MAR-1993

APPLICATION NUMBER: US 07/937,609

FILING DATE: 02-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/928,033

FILING DATE: 11-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/861,769

FILING DATE: 01-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/831,248

FILING DATE: 07-FEB-1992

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 40399/166 NIHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)836-9300

TELEFAX: (703)683-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 2243 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

IMMEDIATE SOURCE:

CLONE: rat brain CCKB receptor

FEATURE:

NAME/KEY: CDS

LOCATION: 136..1494

US-09-443-745-15

Query Match

Best Local Similarity 64.7%; Score 19.4; DB 3; Length 2243;

Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 CATGCTTGTTCAACCGTTCGTCCTGTTTC 29

Db 5 CCGCTTGCTCAACTCTACGCTTGTTTC 33

RESULT 6

US-09-949-016-16262

Sequence 16262, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 16262

LENGTH: 45571

TIPS: DNA

ORGANISM: Human

US-09-949-016-16262

Query Match

63.3%; Score 19; DB 3; Length 45571;

Best Local Similarity 81.5%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TGCTTGTTCACCGTTCGTCTGTTC 29
|| ||||| ||||| ||||| |||||
pb 38119 TGTGTGTTTCATTCGTCTCTCTCTTC 38145

```

RESULT 7
US-09-368-590-1/c
; Sequence 1, Application US/09368590
; Patent No. 6187563
; GENERAL INFORMATION:
; APPLICANT: Solimena, Michele.
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
; ; TITLE OF INVENTION: ANTIGENS OF AUTOIMMUNE DISEASES
; FILE REFERENCE: 101918-200 (OCR-941)
; CURRENT APPLICATION NUMBER: US/09/368,590
; CURRENT FILING DATE: 1999-08-04
; EARLIER APPLICATION NUMBER: 60/095,657
; EARLIER FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 7812
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(6879)
; NAME/KEY: unsure
; LOCATION: (100)...(102)
; NAME/KEY: unsure
; LOCATION: (1021)...(1023)
; NAME/KEY: unsure
; LOCATION: (2266)...(2268)
US-09-368-590-1

```

Query Match 62.7%; Score 18.8; DB 3; Length 7812;
Best Local Similarity 76.7%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 7; Indels 0

Qy 1 CATGCTTGTTCAACCGTTTGGTCTTGTTCCA 30
|||||
Db 841 CATGCTTCTGCAACAGGTGCTGTCCTCCA 812
|||||

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RESULT 8
US-09-949-016-1438/c
; Sequence 1438, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1438
; LENGTH: 8756
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1438
Query Match          62.7%; Score 18.8; DB 3; Length 8756;

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Best Local Similarity	76.7%	Pred. No. 1.3e+02;
Matches	23; Conservative	0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
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Db 1912 CATGCTTCTGCAACAGGTTCGTCTGCTTCCA 1883

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Query Match	62.7%	Score 18.8;	DB 3;	Length 9541;
Best Local Similarity	76.7%	Pred. No. 1.3e+02;		
Matches 23:	Conservative	0;	Mismatches 7;	Indels 0;
	Matches	0;	Gaps	0;

QY 1 CATGCTTGTTCAACCGTTCGTCTGTGCCA 30
 |||||
D6 8049 CAGGCTTGTCCAAAGCTCCATTTTTTCCA 8078
 |||||

RESULT 10
US-09-949-016-13180/c
; Sequence 13180, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-06
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 13180
;; LENGTH: 112874
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)...(112874)
;; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-13180

Query Match 62.7%; Score 18.8; DB 3; Length 112874;
Best Local Similarity 76.7%; Pred. No. 2e+02; 7; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CATCTTGTTCAACCGTTCGTCCTGTTTCCA 30
Db 41167 CATCTTCTGCAACAGGTCTGTCGCTCCA 41138

RESULT 11

US-09-270-767-29480/c
; Sequence 29480, Application US/09270767
; Patent No. 6703491

;; GENERAL INFORMATION:
;; APPLICANT: Homburger et al.
;; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
;; FILE REFERENCE: File Reference: 7326-094
;; CURRENT APPLICATION NUMBER: US/09/270,767
;; CURRENT FILING DATE: 1999-03-17
;; NUMBER OF SEQ ID NOS: 62517
;; SOFTWARE: Patent in Ver. 2.0
;; SEQ ID NO 29480
;; LENGTH: 549
;; TYPE: DNA
;; ORGANISM: *Drosophila melanogaster*

US-09-270-767-29480

Query Match 62.0%; Score 18.6; DB 3; Length 549;
Best Local Similarity 84.0%; Pred. No. 98;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TGCTTGTTCAACCGTTCGTCCTGTT 27
Db 223 TGCTTGTTGAAGAGTCTCTCTGTT 199

RESULT 12

US-09-270-767-13492/c
; Sequence 13492, Application US/09270767
; Patent No. 6703491

;; GENERAL INFORMATION:
;; APPLICANT: Homburger et al.
;; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
;; FILE REFERENCE: File Reference: 7326-094
;; CURRENT APPLICATION NUMBER: US/09/270,767
;; CURRENT FILING DATE: 1999-03-17
;; NUMBER OF SEQ ID NOS: 62517
;; SOFTWARE: Patent in Ver. 2.0
;; SEQ ID NO 13492
;; LENGTH: 1120
;; TYPE: DNA
;; ORGANISM: *Drosophila melanogaster*

US-09-270-767-13492

Query Match 62.0%; Score 18.6; DB 3; Length 1120;
Best Local Similarity 84.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TGCTTGTTCAACCGTTCGTCCTGTT 27
Db 223 TGCTTGTTGAAGAGTCTCTCTGTT 199

RESULT 13

US-09-248-796A-3293
; Sequence 3293, Application US/09248796A
; Patent No. 6747137

;; GENERAL INFORMATION:
;; APPLICANT: Keith Weinstein et al
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN.
;; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: 107196.132
;; CURRENT APPLICATION NUMBER: US/09/248,796A
;; CURRENT FILING DATE: 1999-02-12
;; PRIOR APPLICATION NUMBER: US 60/074,725
;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: US 60/096,409
;; PRIOR FILING DATE: 1998-08-13
;; NUMBER OF SEQ ID NOS: 28208
;; SEQ ID NO 3293
;; LENGTH: 1260
;; TYPE: DNA
;; ORGANISM: *Candida albicans*

US-09-248-796A-3293

Query Match 61.3%; Score 18.4; DB 3; Length 1260;
Best Local Similarity 78.8%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TGCTTGTTCAACCGTTCGTCCTGTTCCA 30
Db 903 TGCTTGTTCAACTGTTGGTGTCCGCCA 930

RESULT 14

US-09-573-080A-7/c
; Sequence 7, Application US/09573080A
; Patent No. 6828097

;; GENERAL INFORMATION:
;; APPLICANT: JOAN KNOLL
;; APPLICANT: ROGAN, PETER

;; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
;; FILE REFERENCE: 30307
;; CURRENT APPLICATION NUMBER: US/09/573,080A
;; CURRENT FILING DATE: 2000-05-16
;; NUMBER OF SEQ ID NOS: 479
;; SOFTWARE: Patent in version 3.0
;; SEQ ID NO 7
;; LENGTH: 2710
;; TYPE: DNA
;; ORGANISM: *Homo sapiens*

;; FEATURE:
;; NAME/KEY: repeat region
;; LOCATION: (1)...(2710)

;; OTHER INFORMATION: charlie3
;; NAME/KEY: misc feature
;; OTHER INFORMATION: n is a, c, g or t
;; PUBLICATION INFORMATION:
;; PUBLICATION INFORMATION:
;; AUTHORS: Jurka, J; Walichewicz, J; Milosavljevic, A
;; TITLE: Prototypic sequences for human repetitive DNA
;; JOURNAL: Journal of Molecular Evolution
;; VOLUME: 35
;; ISSUE: 4
;; PAGES: 286-291
;; DATE: 1992-10-
;; DATABASE ACCESSION NUMBER: Database for repetitive elements (repbase)

;; DATABASE ENTRY DATE: 1996-01-26
;; DATABASE ENTRY DATE: 1996-01-26
US-09-573-080A-7

Query Match 60.7%; Score 18.2; DB 3; Length 2710;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TGCTTGTTCACCGTTCGTCCTGTT 27
Db 1209 TGCTGTTTCACCACTTCGTCCTGTT 1185

RESULT 15
US-09-949-016-200252/c
; Sequence 200252, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200252
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-200252

Query Match 60.0%; Score 18; DB 3; Length 601;
Best Local Similarity 80.8%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 CTGTTTCACCGTTCGTCCTGTTCCA 30
Db 239 CTGTTAAACAGTTCCTGTTGCTCCA 214

Search completed: March 5, 2006, 22:36:22
Job time : 9.38752 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on: March 5, 2006, 23:29:31 ; Search time 43.1372 Seconds
(without alignments)
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Perfect score: 30
Sequence: 1 catgctgttcacacgttcgtctgttcca 30
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084
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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
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3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
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7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	30	100.0	30	US-10-713-381-4	Sequence 4, Appli
2	30	100.0	255	US-10-713-381-9	Sequence 9, Appli
3	30	100.0	1394	US-10-713-381-1	Sequence 1, Appli
4	30	100.0	1394	US-10-713-381-2	Sequence 2, Appli
5	24.2	80.7	158	US-10-713-381-3	Sequence 3, Appli
C 6	22	73.3	1304	US-10-001-857-90	Sequence 90, Appl
C 7	21	70.0	1980090	US-10-719-993-6815	Sequence 6815, Ap
C 8	21	70.0	1980090	US-10-741-600-17676	Sequence 17676, A
9	20.4	68.0	1542	US-09-938-842A-1624	Sequence 1624, Ap
10	20.4	68.0	1542	US-09-938-842A-1624	Sequence 1624, Ap
11	20.2	67.3	2397	US-10-282-122A-31883	Sequence 31883, A
12	20	66.7	2000	US-10-260-238-1785	Sequence 1785, Ap
C 13	19.6	65.3	640	US-10-437-963-96639	Sequence 96639, A
C 14	19.6	65.3	901	US-10-425-115-3534	Sequence 3534, Ap
C 15	19.6	65.3	2000	US-10-260-238-1977	Sequence 1977, Ap
C 16	19.4	64.7	2243	US-09-443-745-15	Sequence 15, Appl
17	19.4	64.7	14655	US-11-063-391-5	Sequence 5, Appli
18	19.4	64.7	2256646	US-10-470-365-1	Sequence 1, Appli
19	19	63.3	822	US-09-925-065A-863989	Sequence 863989,
20	19	63.3	364	US-09-925-065A-546217	Sequence 546217,
C 21	19	63.3	1041	US-10-425-115-100318	Sequence 100318,
C 22	19	63.3	1821	US-10-425-563-5	Sequence 5, Appli
C 23	19	63.3	1821	US-10-972-789A-5	Sequence 5, Appli

C 24	19	63.3	5671	3	US-09-764-872-729	Sequence 729, App
25	19	63.3	198522	5	US-10-087-192-244	Sequence 244, App
C 26	18.8	62.7	520	4	US-09-925-065A-472473	Sequence 472473,
27	18.8	62.7	593	4	US-09-925-065A-936359	Sequence 936359,
28	18.8	62.7	593	4	US-09-925-065A-936360	Sequence 936360,
29	18.8	62.7	593	4	US-09-925-065A-953397	Sequence 953397,
C 30	18.8	62.7	883	3	US-09-934-455-279	Sequence 279, App
C 31	18.8	62.7	883	6	US-10-225-068-183	Sequence 183, App
C 32	18.8	62.7	883	6	US-10-225-068A-971	Sequence 971, App
C 33	18.8	62.7	883	7	US-10-374-780A-381	Sequence 381, App
C 34	18.8	62.7	883	9	US-10-225-068-183	Sequence 183, App
C 35	18.8	62.7	883	9	US-10-225-068A-971	Sequence 971, App
C 36	18.8	62.7	1083	3	US-09-815-242-7281	Sequence 7281, Ap
C 37	18.8	62.7	1083	7	US-10-282-122A-22639	Sequence 22639, A
C 38	18.8	62.7	1083	7	US-10-335-977-2194	Sequence 2194, Ap
C 39	18.8	62.7	1256	7	US-10-437-963-40048	Sequence 40048, A
C 40	18.8	62.7	1856	7	US-10-472-928-2217	Sequence 2217, Ap
C 41	18.8	62.7	1859	8	US-09-815-242-9220	Sequence 9220, Ap
C 42	18.8	62.7	1902	3	US-10-282-122A-37788	Sequence 37788, A
C 43	18.8	62.7	1902	7	US-10-260-238-2535	Sequence 2535, Ap
C 44	18.8	62.7	2000	7	US-10-369-493-33483	Sequence 33483, A
C 45	18.8	62.7	2247	6		

ALIGNMENTS

RESULT 1
US-10-713-381-4
; Sequence 4, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10713381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-4
Query Match 100.0%; Score 30; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.008; 0; Indels 0; Gaps 0;
Matches 30; Conservative 0; Mismatches 0;
Qy 1 CATGCTGTTCACACGTTGCTGTCTTCCA 30
Db 1 CATGCTGTTCACACGTTGCTGTCTTCCA 30
RESULT 2
US-10-713-381-9
; Sequence 9, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME

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; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713.381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-9

Query Match      100.0%; Score 30; DB 8; Length 255;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCAACCGTTCGTCCTTGTTCCA 30
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Db 39 CATGCTTGTTCAACCGTTCGTCCTTGTTCCA 68

RESULT 3
US-10-713-381-1
; Sequence 1, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713.381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-1

Query Match      100.0%; Score 30; DB 8; Length 1394;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCAACCGTTCGTCCTTGTTCCA 30
   |||||
Db 1179 CATGCTTGTTCAACCGTTCGTCCTTGTTCCA 1208

RESULT 4
US-10-713-381-2
; Sequence 2, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713.381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
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; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-2

Query Match      100.0%; Score 30; DB 8; Length 1394;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCAACCGTTCGTCCTTGTTCCA 30
   |||||
Db 1179 CATGCTTGTTCAACCGTTCGTCCTTGTTCCA 1208

RESULT 5
US-10-713-381-3
; Sequence 3, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713.381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 158
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-3

Query Match      80.7%; Score 24.2; DB 8; Length 158;
Best Local Similarity 89.7%; Pred. No. 2.8;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCAACCGTTCGTCCTTGTTCC 29
   |||||
Db 25 CATGCTTGTTCAACCGTTCGTCCTTGTTCC 53

RESULT 6
US-10-001-857-90/c
; Sequence 90, Application US/10001857
; Publication No. US20020183500A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
; FILE REFERENCE: DEX-0273
; CURRENT APPLICATION NUMBER: US/10/001,857
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,054
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 1304
; TYPE: DNA
; ORGANISM: Homo sapien
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US-10-001-857-90

Query Match 73.3%; Score 22; DB 5; Length 1304;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CATGCTTTCACACCGTTCGTCCTGTGTTCCA 30
DB 1155 CTTTCTGTTCCCGCTTCCTCTGTGTTCCA 1126

RESULT 7

US-10-719-993-6815/c
; Sequence 6815, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01496
; CURRENT APPLICATION NUMBER: US/10/719,993
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6815
; LENGTH: 1980090
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1980090)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-719-993-6815

Query Match 70.0%; Score 21; DB 8; Length 1980090;
Best Local Similarity 82.8%; Pred. No. 2.2e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGCTTTCACACCGTTCGTCCTGTGTTCCA 30
DB 1948918 ATTCTGCTGAACAGTTCGTCCTGTGTTACCA 1948890

RESULT 8

US-10-741-600-17676/c
; Sequence 17676, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17676
; LENGTH: 1980090
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1980090)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-17676

Query Match 70.0%; Score 21; DB 8; Length 1980090;
Best Local Similarity 82.8%; Pred. No. 2.2e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGCTTTCACACCGTTCGTCCTGTGTTCCA 30
DB 1948918 ATTCTGCTGAACAGTTCGTCCTGTGTTACCA 1948890

RESULT 9

US-09-938-842A-1624
; Sequence 1624, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1624
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1624

Query Match 68.0%; Score 20.4; DB 3; Length 1542;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CATGCTTGTTCACACCGTTCGTCCTGTGTTCCA 30
DB 237 CATGATTGTTCACCAACATCGTCGTTTCCA 266

RESULT 10

US-09-938-842A-1624
; Sequence 1624, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1624
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1624

Query Match 68.0%; Score 20.4; DB 3; Length 1542;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CATGCTTGTTCACACCGTTCGTCCTGTGTTCCA 30
DB 237 CATGATTGTTCACCAACATCGTCGTTTCCA 266

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RESULT 11
US-10-282-122A-31883
; Sequence 31883, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zvakind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31883
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Pseudomonas putida
US-10-282-122A-31883

Query Match 67.3%; Score 20.2; DB 7; Length 2397;
Best Local Similarity 88.0%; Pred. NO. 2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATGCTTCTTCAACCGTTCGCTTG 25
DB 516 CATGCTGGTACACCGTTCGCTTG 540

RESULT 12
US-10-260-238-1785
; Sequence 1785, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel

```

; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(5322)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 3534
 ; LENGTH: 901
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_103225C.1
 US-10-425-115-3534

Query Match 65.3%; Score 19.6; DB 8; Length 901;
 Best Local Similarity 84.6%; Pred. No. 3.1e+02;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATGCTTTCAACCGTTCGTCGTGT 26
 DB 33 CACGCTTTCAACCGTTCGTCGTGT 8

RESULT 15

US-10-260-238-1977/c
 ; Sequence 1977, Application US/10260238
 ; Publication No. US20040016025A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Budworth, Paul R.
 ; APPLICANT: Moughamer, Todd G.
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Cooper, Bret
 ; APPLICANT: Glazebrook, Jane
 ; APPLICANT: Goff, Stephen A.
 ; APPLICANT: Katagiri, Fumiyaki
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Provatt, Nicholas
 ; APPLICANT: Ricke, Darrell
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
 ; FILE REFERENCE: 60111-NP
 ; CURRENT APPLICATION NUMBER: US/10/260,238
 ; CURRENT FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,448
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,277
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/370,620
 ; PRIOR FILING DATE: 2002-04-04
 ; NUMBER OF SEQ ID NOS: 6077
 ; SEQ ID NO 1977
 ; LENGTH: 2000
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 US-10-260-238-1977

Query Match 65.3%; Score 19.6; DB 7; Length 2000;
 Best Local Similarity 84.6%; Pred. No. 3.4e+02;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 CTGTGTTCAACCGTTCGTCGTTCCTCA 30
 DB 291 CATGTTTAAACCGTTCGTCGTTCCTCA 266

Search completed: March 6, 2006, 03:55:11
 Job time : 47.1372 secs

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Wed Mar 8 14:16:28 2006

us-10-713-381-1_copy_1179_1208.rnpbn

Page 1

GenCore version 5.1.7
Copyright (C) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on: March 6, 2006, 01:58:03 ; Search time 31.3166 Seconds
(without alignments)
2100.307 Million cell updates/sec
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0
Searched: 7218535 seqs, 1096242582 residues
Total number of hits satisfying chosen parameters: 14437070
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:
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3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US03_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
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9: /cgn2_6/ptodata/2/pubpna/US12_NEW_PUB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2.*
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3.*
12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq4.*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.4	64.3	2422	US-11-136-527-2272	Sequence 2272, Ap
2	19	63.7	622	US-09-925-065A-863989	Sequence 863989
3	19	63.3	964	US-09-925-065A-546217	Sequence 546217
C 4	19	63.3	1821	US-11-136-527-2272	Sequence 5, Appl1
5	18.8	62.7	520	US-09-925-065A-472473	Sequence 472473
6	18.8	62.7	593	US-09-925-065A-936359	Sequence 936359
7	18.8	62.7	593	US-09-925-065A-936360	Sequence 936360
8	18.8	62.7	593	US-09-925-065A-953397	Sequence 953397
C 9	18.8	62.7	1908	US-10-523-503-37	Sequence 37, Appl
10	18.8	62.7	128963	US-10-330-773-86	Sequence 86, Appl
11	18.4	61.3	599	US-09-925-065A-811550	Sequence 811550
12	18.4	61.3	624	US-09-925-065A-772237	Sequence 772237
C 13	18.4	61.3	629	US-09-925-065A-787145	Sequence 787145
14	18.4	61.3	642	US-09-925-065A-423	Sequence 423, Appl
15	18.4	61.3	1012	US-10-750-185-52713	Sequence 52713, A
16	18.4	61.3	1012	US-10-750-623-52713	Sequence 52713, A
C 17	18.4	61.3	1257	US-10-750-185-64410	Sequence 64410, A
18	18.4	61.3	1257	US-10-750-623-64410	Sequence 64410, A
C 19	18.4	61.3	1354	US-09-925-065A-70689	Sequence 70689, A
20	18.4	61.3	1354	US-09-925-065A-70689	Sequence 70689, A

C	21	18	60.0	572	6	US-09-925-065A-819344	Sequence 819344,
	22	18	60.0	573	6	US-09-925-065A-821053	Sequence 821053,
	23	18	60.0	1395	6	US-09-925-065A-30378	Sequence 30378, A
	24	18	60.0	1395	6	US-09-925-065A-30379	Sequence 30379, A
	25	17.8	59.3	201	8	US-10-995-561-9774	Sequence 9774, Ap
	26	17.8	59.3	201	8	US-10-995-561-9787	Sequence 9787, Ap
	27	17.8	59.3	201	8	US-10-995-561-52210	Sequence 52210, A
	28	17.8	59.3	603	6	US-09-925-065A-826915	Sequence 826915,
	29	17.8	59.3	617	6	US-09-925-065A-673672	Sequence 673672,
	30	17.8	59.3	617	6	US-09-925-065A-673673	Sequence 673673,
	31	17.8	59.3	652	6	US-09-925-065A-667982	Sequence 667982,
	32	17.8	59.3	1385	6	US-09-925-065A-716810	Sequence 716810,
	33	17.8	59.3	1307	12	US-11-010-239-68	Sequence 68, Appl
	34	17.8	59.3	2039	6	US-09-925-065A-704153	Sequence 704153,
	35	17.8	59.3	2039	6	US-09-925-065A-704154	Sequence 704154,
	36	17.8	59.3	2039	6	US-09-925-065A-704155	Sequence 704155,
	37	17.8	59.3	2867	8	US-10-995-561-357	Sequence 357, App
	38	17.8	59.3	3431	8	US-10-995-561-358	Sequence 358, App
	39	17.8	59.3	9474	12	US-11-155-232-1	Sequence 1, Appl1
	40	17.8	59.3	45038	8	US-10-995-561-13311	Sequence 13311, A
	41	17.8	59.3	81210	8	US-10-995-561-13295	Sequence 13295, A
C	42	17.8	59.3	163317	12	US-11-117-187-212	Sequence 212, App
	43	17.8	59.3	171732	12	US-11-121-086-98	Sequence 98, Appl
	44	17.8	59.3	1082144	12	US-11-117-187-211	Sequence 211, App
	45	17.6	58.7	600	12	US-11-136-527-7828	Sequence 7828, Ap

ALIGNMENTS

RESULT 1
US-11-136-527-2272
; Sequence 2272, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO. 2272
; LENGTH: 2422
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2272

Query Match Best Local Similarity 64.7%; Score 19.4; DB 12; Length 2422;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 CATGCTTGTTCAACCGTGTCTGTGTTCC 29
DB 5 CCTGCTTGCTCAACTCACTGCTGTGTTTC 33

RESULT 2
US-09-925-065A-863989
; Sequence 863989, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24

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; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 863989
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-863989

Query Match      63.3%; Score 19; DB 6; Length 622;
Best Local Similarity 81.5%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  2 ATGCTTGTTCACCGTTCGTTCTTGTTC 28
    ||||| ||||| ||||| ||||| |||||
Db  400 AGGCTAGTCCAACTTTGTCTTGTTC 425

RESULT 3
; US-09-925-065A-546217
; Sequence 546217, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 546217
; LENGTH: 964
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-546217

Query Match      63.3%; Score 19; DB 6; Length 964;
Best Local Similarity 81.5%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  2 ATGCTTGTTCACCGTTCGTTCTTGTTC 28
    ||||| ||||| ||||| ||||| |||||
Db  256 AGGCTAGTCCAACTTTGTCTTGTTC 282

RESULT 4
; US-11-197-133A-5/c
; Sequence 5, Application US/11197133A
; Publication No. US20060040361A1
; GENERAL INFORMATION:
; APPLICANT: De Le Fuente Jose de Jesus
; APPLICANT: Kocan Katherine M.
; APPLICANT: Garcia-Almazan Consuelo
; APPLICANT: Blouin Edwin F.
; TITLE OF INVENTION: Protective antigens and vaccines for the control of multi species
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; TITLE OF INVENTION: Infestations
; FILE REFERENCE: 57338/05-261
; CURRENT APPLICATION NUMBER: US/11/197,133A
; CURRENT FILING DATE: 2005-08-04
; PRIOR APPLICATION NUMBER: US 10/972789
; PRIOR FILING DATE: 2004-10-25
; PRIOR APPLICATION NUMBER: US 10/425563
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/376251
; PRIOR FILING DATE: 2002-04-29
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 1821
; TYPE: DNA
; ORGANISM: Ixodes scapularis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1487)..(1487)
; OTHER INFORMATION: n is a c g o r t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1595)..(1595)
; OTHER INFORMATION: n is a c g o r t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1606)..(1606)
; OTHER INFORMATION: n is a c g o r t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1623)..(1623)
; OTHER INFORMATION: n is a c g o r t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1762)..(1762)
; OTHER INFORMATION: n is a c g o r t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1789)..(1789)
; OTHER INFORMATION: n is a c g o r t
; US-11-197-133A-5

Query Match      63.3%; Score 19; DB 9; Length 1821;
Best Local Similarity 81.5%; Pred. No. 41;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  3 TGGTTGTTCACCGTTCGTTCTTGTTC 29
    ||||| ||||| ||||| ||||| |||||
Db  914 TGGTTCTTGAACCACTTCGTTCTTGTTC 888

RESULT 5
; US-09-925-065A-472473/c
; Sequence 472473, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 472473
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-472473

Query Match 62.7%; Score 18.8; DB 6; Length 520;
Best Local Similarity 76.7%; Pred. No. 37;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 CATGCTTGTTCACCGTTCGTCTGTGTTCCA 30
Db 211 CATGCTTGTTCACCGTTCGTCTGTGTTCCA 182

RESULT 6
US-09-925-065A-936359
; Sequence: 936359, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 936359
; LENGTH: 593
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-936359

Query Match 62.7%; Score 18.8; DB 6; Length 593;
Best Local Similarity 76.7%; Pred. No. 38;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 CATGCTTGTTCACCGTTCGTCTGTGTTCCA 30
Db 341 CATGCTTGTTCACCGTTCGTCTGTGTTCCA 370

RESULT 7
US-09-925-065A-936360
; Sequence: 936360, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 936360
; LENGTH: 593
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-936360

Query Match 62.7%; Score 18.8; DB 6; Length 593;
Best Local Similarity 76.7%; Pred. No. 38;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 CATGCTTGTTCACCGTTCGTCTGTGTTCCA 30
Db 341 CATGCTTGTTCACCGTTCGTCTGTGTTCCA 370

RESULT 8
US-09-925-065A-953397
; Sequence: 953397, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 953397
; LENGTH: 593
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-953397

Query Match 62.7%; Score 18.8; DB 6; Length 593;
Best Local Similarity 76.7%; Pred. No. 38;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 CATGCTTGTTCACCGTTCGTCTGTGTTCCA 30
Db 341 CATGCTTGTTCACCGTTCGTCTGTGTTCCA 370

RESULT 9
US-10-523-503-37/c
; Sequence: 37, Application US/10523503
; Publication No. US20060037102A1
; GENERAL INFORMATION:
; APPLICANT: BASF PLANT SCIENCE GMBH
; TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS IV
; FILE REFERENCE: 16313-0236
; CURRENT APPLICATION NUMBER: US/10/523,503
; CURRENT FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 60/400,803
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 1908

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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-523-503-37

Query Match      62.7%; Score 18.8; DB 7; Length 1908;
Best Local Similarity 76.7%; Pred. No. 51;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CATGCTGTTCAACCGTTCGTCCTGTTCCCA 30
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Db 1688 CTTGCTTCTTCGACCGTGCCTTTTGGTCCA 1659

RESULT 10
US-10-330-773-86/c
; Sequence 86, Application US/10330773
; Publication No. US2006040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 128963
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(128963)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-86

Query Match      62.7%; Score 18.8; DB 7; Length 128963;
Best Local Similarity 76.7%; Pred. No. 1.5e+02;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CATGCTGTTCAACCGTTCGTCCTGTTCCCA 30
    ||||| ||||| ||||| ||||| ||||| |||||
Db 102327 CAAGTTCTTCAACCGTTCCTCATGTACCA 102298

RESULT 11
US-09-925-065A-811550
; Sequence 811550, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 811550
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-811550

Query Match      61.3%; Score 18.4; DB 6; Length 599;
Best Local Similarity 78.6%; Pred. No. 59;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TGGTCTGTTCAACCGTTCGTCCTGTTCCCA 30
    ||||| ||||| ||||| ||||| ||||| |||||
Db 504 TGGTCTGTTCAACCGTTCGTCCTGTTCCCA 531

RESULT 12
US-09-925-065A-772237
; Sequence 772237, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 772237
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-772237

Query Match      61.3%; Score 18.4; DB 6; Length 624;
Best Local Similarity 78.6%; Pred. No. 60;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATGCTGTTCAACCGTTCGTCCTGTTCC 29
    ||||| ||||| ||||| ||||| |||||
Db 49 ATTTTGTCAACTGTCGTCCTGTTTC 76

RESULT 13
US-09-925-065A-787145/c
; Sequence 787145, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 787145
; LENGTH: 629
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-787145

Query Match 61.3%; Score 18.4; DB 6; Length 629;
Best Local Similarity 78.6%; Pred. No. 60;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATGCTTGTTCACCGTTCGTCCTGTTCC 29
Db 576 ATTTTGTTCACCTGTCGTCGTTTC 549

RESULT 14

US-09-925-065A-423
; Sequence 423, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 423
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-423

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Best Local Similarity 78.6%; Pred. No. 60;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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RESULT 15

US-10-750-185-52713
; Sequence 52713, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 52713
; LENGTH: 1012

; TYPE: DNA
; ORGANISM: Bovine 19866881292329
US-10-750-185-52713

Query Match 61.3%; Score 18.4; DB 8; Length 1012;
Best Local Similarity 78.6%; Pred. No. 67;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 454 ATCTTGTTCACCGTTCGTCCTGTTCC 481

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	30	100.0	255	57	US-10-713-381-9
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6	30	100.0	1394	25	US-09-504-487-2
7	30	100.0	1394	57	US-10-713-381-1
8	30	100.0	1394	57	US-10-713-381-2
9	24.2	80.7	158	25	US-09-504-487-3
10	24.2	80.7	158	57	US-10-713-381-3
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21	21.2	70.7	18423	31	US-09-702-134-27508
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28 21 70-0 7201 33 US-09-815-264-77757 Sequence 77757, A
29 21 70-0 7327 38 US-09-620-392-20710 Sequence 20710, A
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c 36 21 70-0 12991 33 US-09-815-264-63656 Sequence 63656, A
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43 21 70-0 27229 28 US-09-620-392-594 Sequence 594, A
44 21 70-0 27229 31 US-09-702-134-25714 Sequence 25714, A
45 21 70-0 27229 33 US-09-815-264-73378 Sequence 73378, A

ALIGNMENTS

RESULT 1
US-09-504-487-4
; Sequence 4, Application US/09504487
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/09/504,487
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Zea mays
US-09-504-487-4
Query Match 100.0%; Score 30; DB 25; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CATGCTTGTTCACCGTTCGCTTGTTCCTCA 30
RESULT 2
US-10-713-381-4
; Sequence 4, Application US/10713381
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381

; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-4
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Best Local Similarity 100.0%; Pred. No. 0.016;
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US-09-504-487-9
; Sequence 9, Application US/09504487
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/09/504,487
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
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; ORGANISM: Zea mays
US-09-504-487-9
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RESULT 4
US-10-713-381-9
; Sequence 9, Application US/10713381
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
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US-10-713-381-9

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DB 39 CATGCTTGTTCAACCGTTCGTCCTGTGTTCCA 68

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US-09-504-487-1
; Sequence 1, Application US/09504487
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE-TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/09/504,487
; CURRENT FILING DATE: 2000-02-15
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; PRIOR FILING DATE: 1997-06-23
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; ORGANISM: Zea mays
US-09-504-487-1

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Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-504-487-2
; Sequence 2, Application US/09504487
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE-TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/09/504,487
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
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; LENGTH: 1394
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US-09-504-487-2

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; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE-TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
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US-10-713-381-1

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Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE-TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
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; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/09/504,487
; CURRENT FILING DATE: 2000-02-15
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; PRIOR FILING DATE: 1997-06-23
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US-09-504-487-3

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; Sequence 3, Application US/10713381
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 158
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-3

Query Match      80.7%; Score 24.2; DB 57; Length 158;
Best Local Similarity 89.7%; Pred. No. 7.5;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCACCGTTCGTCCTTGTTC 29
Db 25 CATGCTTGTTCACCGTTCGTCCTTGTTC 53

RESULT 11
US-10-001-857-90/c
; Sequence 90, Application US/10001857
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Hervé
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
```

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US-09-504-487-3
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
; FILE REFERENCE: DEX-0273
; CURRENT APPLICATION NUMBER: US/10/001,857
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,054
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 1304
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-001-857-90

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Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 1155 CTTCTGTTCCTCCCGTTCCTTGTTC 1126

RESULT 12
US-10-060-063-4003
; Sequence 4003, Application US/10060063
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-Lin
; APPLICANT: Goff, Stephen A.
; TITLE OF INVENTION: CEREAL SIMPLE SEQUENCE REPEAT MARKERS
; FILE REFERENCE: NADII 026A
; CURRENT APPLICATION NUMBER: US/10/060,063
; CURRENT FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 9099
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4003
; LENGTH: 724
; TYPE: DNA
; ORGANISM: RICE
US-10-060-063-4003

Query Match      70.7%; Score 21.2; DB 40; Length 724;
Best Local Similarity 88.5%; Pred. No. 2.1e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTTGTTCAACCGTTCGTCCTTGTTC 30
Db 529 CATGTTTACCGTTCGTCCTTGTTC 554

RESULT 13
US-10-266-090-4003
; Sequence 4003, Application US/10266090
; GENERAL INFORMATION:
; APPLICANT: GORF, STEPHEN
; APPLICANT: BONAN, CAROLINE
; APPLICANT: COLBERT, MICHELLE
; APPLICANT: WANG, RONG-LIN
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; FILE REFERENCE: NADII 058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4003
; LENGTH: 724
; TYPE: DNA
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; ORGANISM: ORYZA SATIVA
US-10-266-090-4003

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Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db      833 CATGTTTAAACCGTTCGTCCTGTTTCCA 858

Search completed: March 6, 2006, 09:38:09
Job time : 270.366 secs

RESULT 14
US-09-702-134-51486
; Sequence 51486, Application US/09702134
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-21(51237)F
; CURRENT APPLICATION NUMBER: US/09/702,134
; CURRENT FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 52202
; SEQ ID NO 51486
; LENGTH: 2221
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-702-134-51486

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Best Local Similarity 88.5%; Pred. No. 2.5e+02;
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RESULT 15
US-09-815-264-109207
; Sequence 109207, Application US/09815264
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Koshi, Jeffrey M.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
; FILE REFERENCE: 38-21(51237)G
; CURRENT APPLICATION NUMBER: US/09/815,264
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 09/702,134
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 109669
; SEQ ID NO 109207
; LENGTH: 2221
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-815-264-109207

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Best Local Similarity 88.5%; Pred. No. 2.5e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 17:38:03 ; Search time 174.564 Seconds
(without alignments)
13025.213 Million cell updates/sec

Title: US-10-713-381-1_COPY_1239_1278

Perfect score: 40

Sequence: 1 agdatacctactcccaaacatccatcttactatgcaac 40

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
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3: gb.env.*
4: gb.cm.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pr.*
9: gb.ro.*
10: gb.sts.*
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12: gb.un.*
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14: gb.hcg.*
15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	40	6	AX224399 Sequence
2	40	100.0	50	6	AX224398 Sequence
3	40	100.0	158	6	AX224396 Sequence
4	40	100.0	255	6	AX224402 Sequence
5	40	100.0	1394	6	BD062176 Male tiss
6	40	100.0	1394	6	BD062177 Male tiss
7	40	100.0	1394	6	AX224394 Sequence
8	40	100.0	1394	6	AX224395 Sequence
9	40	100.0	3343	15	AF360356 Zea mays
10	30.4	76.0	110000	15	AP008209_086 Continuation (87) o
11	30.4	76.0	137327	15	AC135206
12	25.2	63.0	103308	14	AC135670
13	24	60.0	55001	8	AC158670
14	24	60.0	127196	9	AC084230
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16	24	60.0	171940	14	AC148514
17	24	60.0	216548	14	AC161620
18	23.6	59.0	193735	14	AC148501 Callithri

C 19	23.2	58.0	170392	14	AC156784
C 20	23.2	58.0	162616	14	AC160916
C 21	23.2	58.0	211584	9	AC153927
C 22	23	57.5	52648	5	CR788256
C 23	23	57.5	117026	8	AC008897
C 24	23	57.5	153971	9	AC102478
C 25	23	57.5	177104	14	AC125876
C 26	23	57.5	195285	14	CR847932
C 27	23	57.5	218224	9	AC134404
C 28	23	57.5	234163	14	AC115318
C 29	23	57.5	235286	14	AC159385
C 30	23	57.5	242109	14	AC147523
C 31	23	57.5	319056	14	AC016640
C 32	22.8	57.0	164944	2	AC008195
C 33	22.8	57.0	175781	2	AC008091
C 34	22.8	57.0	235928	2	AB003736
C 35	22.8	57.0	309657	14	AC157205
C 36	22.6	56.5	90463	14	AC157458
C 37	22.6	56.5	95896	8	AL356384
C 38	22.6	56.5	129410	14	AC149638
C 39	22.6	56.5	160246	14	AC009221
C 40	22.6	56.5	161817	9	AC132119
C 41	22.6	56.5	170973	8	AP000923
C 42	22.6	56.5	175110	8	AP002428
C 43	22.6	56.5	186457	14	AC129669
C 44	22.6	56.5	196990	14	AC134013
C 45	22.6	56.5	235953	14	AC130117

ALIGNMENTS

RESULT 1
AX224399
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

AX224399 Sequence 6 from Patent WO0160997.
AX224399
AX224399.1 GI:15554641
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1
Albertson,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
Male tissue-preferred regulatory region and method of using same
Patent: WO 0160997-A 6 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
Location/Qualifiers
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ORIGIN

RESULT 2
AX224398
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

AX224398 Sequence 5 from Patent WO0160997.
AX224398
AX224398.1 GI:15554640
Zea mays
Zea mays

Query Match 100.0%; Score 40; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGGATACCTCTCCCAACATCCATCTTACTCATGCAAC 40

ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1
Albertysen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.
Male tissue-preferred regulatory region and method of using same
PATENT: WO 0160997-A 5 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
JOURNAL Location/Qualifiers
FEATURES source
1. .50
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AX224396 158 bp DNA linear PAT 10-SEP-2001
LOCUS
DEFINITION Sequence 3 from Patent WO0160997.
ACCESSION AX224396
VERSION AX224396.1 GI:15554638
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1
Albertysen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.
Male tissue-preferred regulatory region and method of using same
PATENT: WO 0160997-A 3 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
JOURNAL Location/Qualifiers
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Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
AX224402 255 bp DNA linear PAT 10-SEP-2001
LOCUS
DEFINITION Sequence 9 from Patent WO0160997.
ACCESSION AX224402
VERSION AX224402.1 GI:15554644
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1
Albertysen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.
Male tissue-preferred regulatory region and method of using same

JOURNAL Patent: WO 0160997-A 9 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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RESULT 5
BD062176 1394 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Male tissue-preferred regulatory region and method of using same.
ACCESSION BD062176
VERSION BD062176.1 GI:22607781
KEYWORDS JP 2001520523-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 1394)
REFERENCE Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G.A. and
Kendall, T.L.
AUTHORS
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: JP 2001520523-A 1 30-OCT-2001;
PIONEER HI-BRED INTERNATIONAL INC
COMMENT PN JP 2001520523-A/1
PD 30-OCT-2001
PF 19-JUN-1998 JP 1999504910
PR 23-JUN-1997 US 08/880499
PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAT, GARY A HUFFMAN,
TIMMY L KENDALL
PC C12N15/82, C12N15/29, C12N9/24, C12N9/10, C12N9/00 PC
C07K14/34, C12Q1/68,
PC A01H5/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
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RESULT 6
BD062177 1394 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Male tissue-preferred regulatory region and method of using same.
ACCESSION BD062177
VERSION BD062177.1 GI:22607782
KEYWORDS JP 2001520523-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1394)

Albertsen M.C., Fox, T.W., Garnaat, C.W., Huffman, G.A. and Kendall, T.L.

Male tissue-preferred regulatory region and method of using same

PIONEER HI-BRED INTERNATIONAL INC

JP 2001520523-A/2

30-OCT-2001

19-JUN-1998 JP 1999504910

23-JUN-1997 US 08/880499

MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAAT, GARY A HUFFMAN, TIMMY L KENDALL

C12N15/82, C12N15/29, C12N9/24, C12N9/22, C12N9/10, C12N9/00 PC

, C07K14/34, C12Q1/68,

A01H5/00

Strandedness: Single;

Topology: Linear;

Key Location/Qualifiers.

PH Key Location/Qualifiers

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LOCUS 1394 bp DNA linear PAT 10-SEP-2001

DEFINITION Sequence 1 from Patent WO0160997.

ACCESSION AX224394

VERSION AX224394.1 GI:15554636

KEYWORDS Zea mays

SOURCE Zea mays

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1

Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.

Male tissue-preferred regulatory region and method of using same

PIONEER HI-BRED INTERNATIONAL, INC. (US)

Location/Qualifiers

1. 1394

/organism="Zea mays"

/mol_type="unassigned DNA"

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Query Match 100.0%; Score 40; DB 6; Length 1394;

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RESULT 8

AX224395

LOCUS 1394 bp DNA linear PAT 10-SEP-2001

DEFINITION Sequence 2 from Patent WO0160997.

ACCESSION AX224395

VERSION AX224395.1 GI:15554637

KEYWORDS Zea mays

SOURCE Zea mays

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1

Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.

Male tissue-preferred regulatory region and method of using same

PIONEER HI-BRED INTERNATIONAL, INC. (US)

Location/Qualifiers

1. 1394

/organism="Zea mays"

/mol_type="unassigned DNA"

/db_xref="taxon:4577"

Query Match 100.0%; Score 40; DB 6; Length 1394;

Best Local Similarity 100.0%; Pred. No. 6.2e-05;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278

RESULT 9

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LOCUS 3343 bp DNA linear PIN 12-MAY-2001

DEFINITION Zea mays male fertility protein (Me45) gene, complete cds.

ACCESSION AF360356

VERSION AF360356.1 GI:14028756

KEYWORDS Zea mays

SOURCE Zea mays

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 3343)

Fox, T.W., Trimmell, M.R. and Albertsen, M.C.

Cloning of Me45, a gene required for male fertility from Zea mays

Unpublished

2 (bases 1 to 3343)

Fox, T.W., Trimmell, M.R. and Albertsen, M.C.

Direct Submission

Submitted (13-MAR-2001) Trait and Technology Development; Pioneer HI-Bred Intl. Inc., 7300 N.W. 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA

Location/Qualifiers

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1394)

Albertsen M.C., Fox, T.W., Garnaat, C.W., Huffman, G.A. and Kendall, T.L.

Male tissue-preferred regulatory region and method of using same

PIONEER HI-BRED INTERNATIONAL INC

JP 2001520523-A/2

30-OCT-2001

19-JUN-1998 JP 1999504910

23-JUN-1997 US 08/880499

MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAAT, GARY A HUFFMAN, TIMMY L KENDALL

C12N15/82, C12N15/29, C12N9/24, C12N9/22, C12N9/10, C12N9/00 PC

, C07K14/34, C12Q1/68,

A01H5/00

Strandedness: Single;

Topology: Linear;

Key Location/Qualifiers.

PH Key Location/Qualifiers

1. 1394

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

Query Match 100.0%; Score 40; DB 6; Length 1394;

Best Local Similarity 100.0%; Pred. No. 6.2e-05;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40

Db 1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278

RESULT 7

AX224394

LOCUS 1394 bp DNA linear PAT 10-SEP-2001

DEFINITION Sequence 1 from Patent WO0160997.

ACCESSION AX224394

VERSION AX224394.1 GI:15554636

KEYWORDS Zea mays

SOURCE Zea mays

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1

Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.

Male tissue-preferred regulatory region and method of using same

PIONEER HI-BRED INTERNATIONAL, INC. (US)

Location/Qualifiers

1. 1394

/organism="Zea mays"

/mol_type="unassigned DNA"

/db_xref="taxon:4577"

Query Match 100.0%; Score 40; DB 6; Length 1394;

Best Local Similarity 100.0%; Pred. No. 6.2e-05;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40

Db 1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278

RESULT 8

AX224395

LOCUS 1394 bp DNA linear PAT 10-SEP-2001

DEFINITION Sequence 2 from Patent WO0160997.

ACCESSION AX224395

VERSION AX224395.1 GI:15554637

KEYWORDS Zea mays

SOURCE Zea mays

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1

Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.

Male tissue-preferred regulatory region and method of using same

PIONEER HI-BRED INTERNATIONAL, INC. (US)

Location/Qualifiers

1. 1394

/organism="Zea mays"

/mol_type="unassigned DNA"

/db_xref="taxon:4577"

Query Match 100.0%; Score 40; DB 6; Length 1394;

Best Local Similarity 100.0%; Pred. No. 6.2e-05;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40

Db 1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278

RESULT 9

AF360356

LOCUS 3343 bp DNA linear PIN 12-MAY-2001

DEFINITION Zea mays male fertility protein (Me45) gene, complete cds.

ACCESSION AF360356

VERSION AF360356.1 GI:14028756

KEYWORDS Zea mays

SOURCE Zea mays

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 3343)

Fox, T.W., Trimmell, M.R. and Albertsen, M.C.

Cloning of Me45, a gene required for male fertility from Zea mays

Unpublished

2 (bases 1 to 3343)

Fox, T.W., Trimmell, M.R. and Albertsen, M.C.

Direct Submission

Submitted (13-MAR-2001) Trait and Technology Development; Pioneer HI-Bred Intl. Inc., 7300 N.W. 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA

Location/Qualifiers

1. 3343

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="B73"

/db_xref="taxon:4577"

/chromosome="9L"

<1392..>2942

/gene="Me45"

Join(<1392..1768,1898..2182,2280..2447,2534..>2942)

/gene="Me45"

/product="male fertility protein"

Join(11392..1768,1898..2182,2280..2447,2534..2942)

/gene="Me45"

/codon_start=1

/product="male fertility protein"

/protein_id="AAK52489.1"

/db_xref="GI:14028757"

/translation="MEKENLQWRGRDGIQVPHLFAALALALIVADPFLSPLAEV DYRVPYHELAPYGVGWSNPRDRLEFVGFQPSIEFDLQQRGYAGLA DGRVVRWNGEAGWETFAVWNPDSVCANGVNSTTRKHKEBFQCRPLGLRPHGE

TGELYVADAYVGLMVQSGVASSVAREADGPIRFANDLDVHRNGSVFFFTDTSMRY
SRDHLNILLGEGTGELLYRDEPETSQVHVVLKGLVPPNGVOISQEDHQELLSEFTTNC
RIMRYLEGGPRAGEVEFANLPGFNDVRNQRGQFWAIDCCRTPAQEVFAKRPWIR
TLYFKFLSLKVLVTWKAARMHTVYLLALLDGEGRVVEVLEDRGHEVMKLVSEVREVGK
LWIGTVAHNHIATPYPLED"

ORIGIN

Query Match 100.0%; Score 40; DB 15; Length 3343;
Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40
|||||
Db 1239 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 1278

RESULT 10
AP008209_086/c

WPCOMMENT

Sequence split into 362 fragments LOCUS AP008209 Accession AP008209

Fragment Name	Begin	End
AP008209_000	1	110000
AP008209_001	100001	210000
AP008209_002	200001	310000
AP008209_003	300001	410000
AP008209_004	400001	510000
AP008209_005	500001	610000
AP008209_006	600001	710000
AP008209_007	700001	810000
AP008209_008	800001	910000
AP008209_009	900001	1010000
AP008209_010	1000001	1110000
AP008209_011	1100001	1210000
AP008209_012	1200001	1310000
AP008209_013	1300001	1410000
AP008209_014	1400001	1510000
AP008209_015	1500001	1610000
AP008209_016	1600001	1710000
AP008209_017	1700001	1810000
AP008209_018	1800001	1910000
AP008209_019	1900001	2010000
AP008209_020	2000001	2110000
AP008209_021	2100001	2210000
AP008209_022	2200001	2310000
AP008209_023	2300001	2410000
AP008209_024	2400001	2510000
AP008209_025	2500001	2610000
AP008209_026	2600001	2710000
AP008209_027	2700001	2810000
AP008209_028	2800001	2910000
AP008209_029	2900001	3010000
AP008209_030	3000001	3110000
AP008209_031	3100001	3210000
AP008209_032	3200001	3310000
AP008209_033	3300001	3410000
AP008209_034	3400001	3510000
AP008209_035	3500001	3610000
AP008209_036	3600001	3710000
AP008209_037	3700001	3810000
AP008209_038	3800001	3910000
AP008209_039	3900001	4010000
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AP008209_041	4100001	4210000
AP008209_042	4200001	4310000
AP008209_043	4300001	4410000
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AP008209_046	4600001	4710000
AP008209_047	4700001	4810000
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AP008209_049	4900001	5010000
AP008209_050	5000001	5110000
AP008209_051	5100001	5210000

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AP008209_125 12500001 12610000
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 AP008209_192 19200001 19310000
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 AP008209_196 19600001 19710000

Query Match. 76.0%; Score 30.4; DB 15; Length 110000;
 Best Local Similarity 85.0%; Pred. No. 0.18;
 Matches 34; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 AGGATACCTACTCCCAACATTCATCTTACTCATGCAAC 40
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 Db 36341 AGAACACCTACTCCCAACATTCACGCTGACTCATGCAAC 36302
 |||||

RESULT 11
 AC135206/c 137327 bp DNA linear PLN 16-APR-2003
 LOCUS Oryza sativa (japonica cultivar-group) chromosome 3 clone
 Q31041802, complete sequence.

ACCESSION AC135206.3 GI:27596977
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 137327)
 AUTHORS Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Currie, J. and Collura, K.

TITLE Rice Genomic Sequence
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 137327)
 AUTHORS Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Saski, C., Currie, J., Collura, K. and Thompson, S.

TITLE Direct Submission
 JOURNAL Submitted (09-OCT-2002) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA

REFERENCE 3 (bases 1 to 137327)
 AUTHORS Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Saski, C., Currie, J., Collura, K. and Thompson, S.

TITLE Direct Submission
 JOURNAL Submitted (06-NOV-2002) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA

REFERENCE 4 (bases 1 to 137327)
 AUTHORS Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Currie, J., Collura, K. and Thompson, S.

TITLE Direct Submission
 JOURNAL Submitted (11-JAN-2003) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA

REFERENCE 5 (bases 1 to 137327)
 AUTHORS Wing, R.A., Yu, Y., Soderlund, C., Chen, M., Kim, H., Rambo, T., Saski, C., Henry, D., Thompson, S., Simmons, J., Thurmond, S.K. and Sun, S.

TITLE Direct Submission
 JOURNAL Submitted (16-APR-2003) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA

COMMENT On Jan 11, 2003 this sequence version replaced gi:24635891.
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by more than one plasmid subclone; and the assembly was confirmed by restriction digest. There are transposons located at area 29427-32874 and at area 19945-33212. Region 70511-70536 is covered by a single subclone. Region 18678-18873 is a double stranded single subclone. Areas 69857-70761, 89836-90416, 98951-99009, 105316-105607, and 133052-133152 are covered by Monsanto only. The nucleotide sequence of this BAC clone was generated by combining Syngenta, Monsanto and Arizona Genomics Institute sequencing data.

FEATURES
 source
 1. 137327
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="genomic DNA"
 /db_xref="taxon:39947"
 /chromosome="3"
 /clone="OU1041F02"

RESULT 12
AC156670
LOCUS
DEFINITION
AC156670.2 GI:68266432
VERSION
KEYWORDS
SOURCE
ORGANISM

AC156670 303308 bp DNA linear HTG 01-JUL-2005
Bos taurus clone CH240-60K24, *** SEQUENCING IN PROGRESS ***, 48
unordered pieces.

AC156670
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Bos taurus (cow)

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

3 (bases 1 to 303308)
Cow Genome Sequencing Consortium.
Submitted (01-JUL-2005) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jun 28, 2005 this sequence version replaced gi:58531390.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: FDUU
Center clone name: CH240-60K24
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 284059 bases at least Q40
Consensus quality: 288397 bases at least Q30
Consensus quality: 292413 bases at least Q20
Estimated insert size: 289468; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 48 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 4448: contig of 4448 bp in length
* 4498: gap of 50 bp
* 4499: contig of 9745 bp in length
* 14243: gap of 50 bp
* 14244: contig of 21076 bp in length
* 14293: gap of 50 bp
* 35369: contig of 21076 bp in length
* 35419: gap of 50 bp
* 35420: contig of 12086 bp in length
* 47505: gap of 50 bp
* 47506: contig of 1877 bp in length
* 47556: gap of 50 bp
* 49433: contig of 2133 bp in length
* 49482: gap of 50 bp
* 51615: contig of 6917 bp in length
* 52521: gap of 906 bp
* 59438: contig of 5333 bp in length
* 59488: gap of 50 bp
* 64821: contig of 50 bp
* 64822: gap of 50 bp
* 64871: contig of 9669 bp in length
* 74540: contig of 9669 bp in length
* 74541: gap of 50 bp
* 74590: contig of 15770 bp in length
* 90361: gap of 473 bp
* 90833: contig of 9213 bp in length
* 100046: contig of 50 bp
* 100096: gap of 50 bp
* 100097: contig of 4554 bp in length
* 104650: contig of 300 bp
* 104950: gap of 1500 bp in length
* 106451: contig of 158 bp
* 106608: gap of 3179 bp in length
* 109787: contig of 3179 bp in length

gc-helpobcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:
http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

QUALSTAT-REPORT.

FEATURES	Location/Qualifiers
source	1..55001 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="12" /clone="RP11-568G5"
misc_feature	1..1301 /note="overlaps bases 177088..178398 of clone AC079630" /function="Clone overlap"
repeat_region	35..229 /rpt_family="MIR"
repeat_region	1002..1023 /rpt_family="AT-rich"
repeat_region	1092..1227 /rpt_family="MIR"
repeat_region	complement(2156..2209) /rpt_family="L2"
repeat_region	3563..3650 /rpt_family="(CCGTA)n"
repeat_region	complement(3698..3765) /rpt_family="L2"
repeat_region	complement(3840..3908) /rpt_family="L1MD3"
repeat_region	complement(4234..4464) /rpt_family="MIR"
repeat_region	complement(4847..4914) /rpt_family="MIR"
repeat_region	4938..5053 /rpt_family="L2"
repeat_region	6350..6660 /rpt_family="AluSg"
repeat_region	complement(7309..7743) /rpt_family="LTR43"
repeat_region	7744..9144 /rpt_family="L1PA4"

repeat_region	complement(9151..9317)
repeat_region	/rpt_family="LTR43"
repeat_region	10587..10846 /rpt_family="L1M4"
repeat_region	10912..11015 /rpt_family="L1P"
repeat_region	11098..11271 /rpt_family="L1ME"
repeat_region	11450..11535 /rpt_family="MLTII"
repeat_region	11941..12179 /rpt_family="MIR"
repeat_region	12797..12828 /rpt_family="(CATATA)n"
repeat_region	complement(12975..13087) /rpt_family="FLAM_C"
repeat_region	13714..13737 /rpt_family="AT-rich"
repeat_region	14058..14219 /rpt_family="MER45"
repeat_region	14411..14545 /rpt_family="MIR"
repeat_region	complement(15058..15127) /rpt_family="MIR"
repeat_region	16186..16413 /rpt_family="MIR"
repeat_region	complement(17624..17922) /rpt_family="AluJb"
repeat_region	complement(18309..18606) /rpt_family="AluSx"
repeat_region	18844..18854 /rpt_family="AT-rich"
repeat_region	complement(18855..19135) /rpt_family="AluJb"
repeat_region	19136..19158 /rpt_family="AT-rich"
repeat_region	complement(20660..20753) /rpt_family="MER91C"
repeat_region	22179..22680 /rpt_family="(TAAAA)n"
repeat_region	22180..22358 /rpt_family="AluJb"
repeat_region	22359..22632 /rpt_family="AluJb"
repeat_region	22833..22860 /rpt_family="(TAAAA)n"
repeat_region	22882..22789 /rpt_family="AluJb"
repeat_region	22796..23099 /rpt_family="AluY"
repeat_region	complement(23147..23327)

Query Match 60.0%; Score 24; DB 8; Length 55001;
Best Local Similarity 84.4%; Pred. No. 62;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 ATACTTACTCCCAACATCCATCTTACTCAT 35
Db 47598 AACTTACTCCCAACATCTTACTCAT 47567

RESULT 14
AL807784/c. 127196 bp DNA linear ROD 13-NOV-2002
LOCUS Mouse DNA sequence from clone RP23-448C18 on chromosome X, complete
DEFINITION sequence.
ACCESSION AL807784
VERSION AL807784.11 GI:25045332
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Best Local Similarity 84.4%; Pred. No. 53;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 ATACCTACTCCAAACAATCCATCTTACTCAT 35
| | | | | | | | | | | | | | | | | | | | | |
Db 123632 AACTTACTCCAAACAATCTATGTCACTCAT 123663

Search completed: March 5, 2006, 21:55:41
Job time : 179.689 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 17:08:23 ; Search time 26.619 Seconds
(without alignments)
10014.946 Million cell updates/sec

Title: US-10-713-381-1_COPY_1239_1278

Perfect score: 40
Sequence: 1 aggatacttactcccaaacatccatcttactatgcaac 40

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Geneseq 21.*
- 2: Geneseq 1990s.*
- 3: Geneseq 2000s.*
- 4: Geneseq 2001as.*
- 5: Geneseq 2001bs.*
- 6: Geneseq 2002as.*
- 7: Geneseq 2002bs.*
- 8: Geneseq 2003as.*
- 9: Geneseq 2003bs.*
- 10: Geneseq 2003cs.*
- 11: Geneseq 2003ds.*
- 12: Geneseq 2004as.*
- 13: Geneseq 2004bs.*
- 14: Geneseq 2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	40	5	Aah76337 Z. mays M
2	40	100.0	50	5	Aah76336 Z. mays M
3	40	100.0	158	5	Aah76334 Z. mays M
4	40	100.0	255	5	Aah76340 Z. mays M
5	40	100.0	1394	2	Aax07408 Zea mays
6	40	100.0	1394	2	Aax07409 Zea mays
7	40	100.0	1394	5	Aah76332 Z. mays M
8	40	100.0	1394	5	Aah76333 Z. mays M
9	30.4	78.0	2000	11	Ac138730 Rice stre
10	22.4	56.0	226215	11	Acn45146 Human Gen
11	21.6	54.0	4110	8	Abz10202 Haematopo
12	21.6	54.0	6309	6	Abz13204 Human imm
13	21.6	54.0	7110	10	Abz54282 Pretreat
14	21.6	54.0	7110	10	Abz54282 Pretreat
15	21.6	54.0	7110	13	Ades4196 Human lym
16	21.6	54.0	1341	13	Ades9580 Oligonuc
17	21.4	53.5	1341	6	Abz13750 Arabidops
18	21.4	53.5	6681	6	Abz132155 Human
19	21.4	53.5	6681	6	Abz154304 Chemical
20	21.4	53.5	8168	6	Abz132928 Human imm

C 20	21.4	53.5	8168	6	AAS63328
C 21	21.4	53.5	24401	4	ABL03396
C 22	21	52.5	1531	14	ADM17938
C 23	21	52.5	2000	11	ACL35665
C 24	21	52.5	2000	12	ADJ41594
C 25	21	52.5	2792	12	ADM98941
C 26	21	52.5	3117	12	ADM98942
C 27	21	52.5	5507	8	ABZ10204
C 28	21	52.5	5507	8	ABZ10058
C 29	21	52.5	8404	4	AAS46500
C 30	21	52.5	8404	6	ABL33595
C 31	21	52.5	8404	10	ADS54216
C 32	21	52.5	8404	10	ADS4088
C 33	21	52.5	8404	10	ADE84076
C 34	21	52.5	8404	10	ADE84152
C 35	21	52.5	8404	13	ADS89242
C 36	21	52.5	8404	13	ADS89516
C 37	21	52.5	10286	4	AAS45308
C 38	21	52.5	10286	6	ABK28147
C 39	21	52.5	63115	10	ADC85419
C 40	21	52.5	63294	9	ADA02939
C 41	21	52.5	63294	10	ADB72677
C 42	21	52.5	63294	12	ADM74534
C 43	21	52.5	106315	11	ACN43966
C 44	20.8	52.0	891	8	ABZ51893
C 45	20.8	52.0	6620	4	AAS45488

ALIGNMENTS

RESULT 1

AAH76337
ID AAH76337 standard; DNA; 40 BP.

AC AAH76337;

DT 29-OCT-2001 (first entry)

DE Z. mays Ms45 male tissue-preferred regulatory region fragment.

DE Ms45; male tissue; regulatory region; transcription; male fertility;

KW hybrid seed; ds.

OS Zea mays.

PN WO200160997-A2.

PD 23-AUG-2001.

PF 13-FEB-2001; 2001MO-US004527.

PR 15-FEB-2000; 2000US-00504487.

XX (PION-) PIONEER HI-BRED INT INC.

XX Albertsen MC, Fox TW, Garmaat CW, Huffman G, Kendall TL;

XX WPI; 2001-514772/56.

XX A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the Ms45 gene useful for

XX Claim 14; Page 32; 50pp; English.

XX The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the Ms45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The

CC present sequence represents a DNA fragment upstream of the TATA box of a
CC Z. mays Ms45 male-tissue preferred regulatory region nucleotide sequence
XX
SQ Sequence 40 BP; 14 A; 14 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 40; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40
|||||
Db 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40
|||||

RESULT 2

AAH76336
ID AAH76336 standard; DNA; 50 BP.

XX
AC AAH76336;

XX
DT 29-OCT-2001 (first entry)

XX Z. mays Ms45 male tissue-preferred regulatory region fragment.

XX Ms45; male tissue; regulatory region; transcription; male fertility;
XX hybrid seed; ds.

XX Zea mays.

XX WO200160997-A2.

XX 23-AUG-2001.

XX 13-FEB-2001; 2001WO-US004527.

XX 15-FEB-2000; 2000US-00504487.

XX (PION-) PIONEER HI-BRED INT INC.

XX Albertsen MC, Fox TW, Garmaat CW, Huffman G, Kendall TL;

XX WPI; 2001-514772/56.

XX A male tissue-preferred regulatory region comprising nucleotide sequences
XX essential for initiating transcription of the MS45 gene useful for
XX mediating fertility in a male plant.

XX Claim 5; Page 47; 50pp; English.

XX The invention provides a male tissue-preferred regulatory region (I)
XX comprising nucleotide sequences essential for initiating transcription of
XX the MS45 gene. A method of mediating male fertility in a plant is
XX provided that involves introducing an expression vector comprising a
XX promoter operably linked to (I) into a plant where the exogenous gene
XX impacts male fertility of the plant and (I) controls expression of the
XX exogenous gene. A method of producing hybrid seeds is also provided. The
XX present sequence represents a DNA fragment -72 to -111 bases upstream of
XX the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region
XX nucleotide sequence

XX Sequence 50 BP; 18 A; 17 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 40; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40
|||||
Db 11 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 50
|||||

RESULT 3

AAH76334

ID AAH76334 standard; DNA; 158 BP.

XX
AC AAH76334;

XX
DT 29-OCT-2001 (first entry)

XX Z. mays Ms45 male tissue-preferred regulatory region fragment.

XX Ms45; male tissue; regulatory region; transcription; male fertility;
XX hybrid seed; ds.

XX Zea mays.

XX WO200160997-A2.

XX 23-AUG-2001.

XX 13-FEB-2001; 2001WO-US004527.

XX 15-FEB-2000; 2000US-00504487.

XX (PION-) PIONEER HI-BRED INT INC.

XX Albertsen MC, Fox TW, Garmaat CW, Huffman G, Kendall TL;

XX WPI; 2001-514772/56.

XX A male tissue-preferred regulatory region comprising nucleotide sequences
XX essential for initiating transcription of the MS45 gene useful for
XX mediating fertility in a male plant.

XX Claim 5; Page 47; 50pp; English.

XX The invention provides a male tissue-preferred regulatory region (I)
XX comprising nucleotide sequences essential for initiating transcription of
XX the MS45 gene. A method of mediating male fertility in a plant is
XX provided that involves introducing an expression vector comprising a
XX promoter operably linked to (I) into a plant where the exogenous gene
XX impacts male fertility of the plant and (I) controls expression of the
XX exogenous gene. A method of producing hybrid seeds is also provided. The
XX present sequence represents a DNA fragment -38 to -195 bases upstream of
XX the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region
XX nucleotide sequence

XX Sequence 158 BP; 41 A; 50 C; 21 G; 46 T; 0 U; 0 Other;

Query Match 100.0%; Score 40; DB 5; Length 158;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40
|||||
Db 86 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 125
|||||

RESULT 4

AAH76340

ID AAH76340 standard; DNA; 255 BP.

XX
AC AAH76340;

XX
DT 29-OCT-2001 (first entry)

XX Z. mays Ms45 promoter fragment.

XX Ms45; male tissue; regulatory region; transcription; male fertility;
XX hybrid seed; promoter; ds.

XX Zea mays.

XX WO200160997-A2.

XX 23-AUG-2001.

XX PF 13-FEB-2001; 2001WO-US004527.
 XX PR 15-FEB-2000; 2000US-00504487.
 XX PA (PION-) PIONEER HI-BRED INT INC.
 XX PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
 XX WPI; 2001-514772/56.
 XX A male tissue-preferred regulatory region comprising nucleotide sequences
 PT essential for initiating transcription of the Ms45 gene useful for
 PT mediating fertility in a male plant.
 XX Example 5; Fig 8; 50pp; English.
 XX The invention provides a male tissue-preferred regulatory region (I)
 CC comprising nucleotide sequences essential for initiating transcription of
 CC the Ms45 gene. A method of mediating male fertility in a plant is
 CC provided that involves introducing an expression vector comprising a
 CC promoter operably linked to (I) into a plant where the exogenous gene
 CC impacts male fertility of the plant and (I) controls expression of the
 CC exogenous gene. A method of producing hybrid seeds is also provided. The
 CC present sequence represents a Z. mays Ms45 promoter fragment
 XX
 XX SQ Sequence 255 BP; 59 A; 86 C; 39 G; 71 T; 0 U; 0 Other;
 Query Match 100.0%; Score 40; DB 5; Length 255;
 Best Local Similarity 100.0%; Pred. No. 5.3e-06;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40
 DB 99 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 138
 RESULT 5
 AAX07408
 ID AAX07408 standard; DNA; 1394 BP.
 XX AAX07408;
 XX 08-JUN-1999 (first entry)
 XX Zea mays Ms45 male tissue-preferred regulatory region.
 XX Ms45; male; tissue-preferred; regulatory region; plant cells;
 XX Plant tissue; differentiated; maize; hybrid seed; fertility; ss.
 XX Zea mays.
 XX WO9859061-A1.
 XX 30-DEC-1998.
 XX 19-JUN-1996; 98WO-US012895.
 XX 23-JUN-1997; 97US-00880499.
 XX (PION-) PIONEER HI-BRED INT INC.
 XX Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
 XX WPI; 1999-105628/09.
 XX New nucleic acid encoding a Ms45 male tissue-preferred regulatory region
 PT - useful in mediating plant fertility, especially hybrid seed production.
 XX Claim 2; Page 22-23; 39pp; English.
 XX The sequence is that encoding an Ms45 male tissue-preferred regulatory
 CC region. It may be used in the construction of a vector for a method of

CC producing exogenous genes in a male tissue-preferred manner, which is
 CC useful in restoring or conferring fertility, such as in hybrid seed
 CC production. In conferring fertility, a monocot/dicot plant is transformed
 CC with the exogenous nucleotide sequence (a male sterility gene, preferably
 CC Ms45), which encodes a product selected from auxins, rolB and diptheria
 CC toxin. Hybrid seeds are produced by cross-pollinating maize male fertile
 CC and infertile plants
 XX
 XX SQ Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
 Query Match 100.0%; Score 40; DB 2; Length 1394;
 Best Local Similarity 100.0%; Pred. No. 6.8e-06;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40
 DB 1239 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 1278
 RESULT 6
 AAX07409
 ID AAX07409 standard; DNA; 1394 BP.
 XX AAX07409;
 XX 08-JUN-1999 (first entry)
 XX Zea mays Ms45 male tissue-preferred regulatory region.
 XX Ms45; male; tissue-preferred; regulatory region; plant cells;
 XX Plant tissue; differentiated; hybrid seed; fertility; ss.
 XX Zea mays.
 XX WO9859061-A1.
 XX 30-DEC-1998.
 XX 19-JUN-1996; 98WO-US012895.
 XX 23-JUN-1997; 97US-00880499.
 XX (PION-) PIONEER HI-BRED INT INC.
 XX Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
 XX WPI; 1999-105628/09.
 XX New nucleic acid encoding a Ms45 male tissue-preferred regulatory region
 PT - useful in mediating plant fertility, especially hybrid seed production.
 XX Claim 3; Page 23-24; 39pp; English.
 XX The sequence is that encoding an Ms45 male tissue-preferred regulatory
 CC region. It may be used in the construction of a vector for a method of
 CC producing exogenous genes in a male tissue-preferred manner, which is
 CC useful in restoring or conferring fertility, such as in hybrid seed
 CC production. In conferring fertility, a monocot/dicot plant is transformed
 CC with the exogenous nucleotide sequence (a male sterility gene, preferably
 CC Ms45), which encodes a product selected from auxins, rolB and diptheria
 CC toxin. Hybrid seeds are produced by cross-pollinating maize male fertile
 CC and infertile plants
 XX
 XX SQ Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;
 Query Match 100.0%; Score 40; DB 2; Length 1394;
 Best Local Similarity 100.0%; Pred. No. 6.8e-06;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40
 DB 1239 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 1278

```

RESULT 7
AAH76332
ID AAH76332 standard; DNA; 1394 BP.
XX
XX AC AAH76332;
XX
XX DT 29-OCT-2001 (first entry)
XX
XX DE Z. mays Ms45 male tissue-preferred regulatory region encoding DNA.
XX
XX KW Ms45; male tissue; regulatory region; transcription; male fertility;
XX
XX KW hybrid seed; ds.
XX
XX OS Zea mays.
XX
XX PN WO200160997-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 13-FEB-2001; 2001WO-US004527.
XX
XX PR 15-FEB-2000; 2000US-00504487.
XX
XX PA (PION-) PIONEER HI-BRED INT INC.
XX
XX PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
XX
XX DR WPI; 2001-514772/56.
XX
XX PT A male tissue-preferred regulatory region comprising nucleotide sequences
XX
XX KW essential for initiating transcription of the Ms45 gene useful for
XX
XX OS mediating fertility in a male plant.
XX
XX PN Claim 4; Page 46; 50pp; English.
XX
XX CC The invention provides a male tissue-preferred regulatory region (I)
XX
XX CC comprising nucleotide sequences essential for initiating transcription of
XX
XX CC the Ms45 gene. A method of mediating male fertility in a plant is
XX
XX CC provided that involves introducing an expression vector comprising a
XX
XX CC promoter operably linked to (I) into a plant where the exogenous gene
XX
XX CC impacts male fertility of the plant and (I) controls expression of the
XX
XX CC exogenous gene. A method of producing hybrid seeds is also provided. The
XX
XX CC present sequence represents a nucleic acid sequence encoding an Ms45 male
XX
XX CC -tissue preferred regulatory region from Z. mays
XX
XX SQ Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 40; DB 5; Length 1394;
XX
XX Best Local Similarity 100.0%; Pred. No. 6.8e-06;
XX
XX Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
XX
XX DB 1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278
XX
XX
XX RESULT 8
AAH76333
ID AAH76333 standard; DNA; 1394 BP.
XX
XX AC AAH76333;
XX
XX XX 29-OCT-2001 (first entry)
XX
XX DE Z. mays Ms45 male tissue-preferred regulatory region encoding DNA.
XX
XX KW Ms45; male tissue; regulatory region; transcription; male fertility;
XX
XX KW hybrid seed; ds.
XX
XX OS Zea mays.
XX
XX PN WO200160997-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 13-FEB-2001; 2001WO-US004527.
XX
XX PR 15-FEB-2000; 2000US-00504487.
XX
XX PA (PION-) PIONEER HI-BRED INT INC.
XX
XX PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
XX
XX DR WPI; 2001-514772/56.
XX
XX PT A male tissue-preferred regulatory region comprising nucleotide sequences
XX
XX KW essential for initiating transcription of the Ms45 gene useful for
XX
XX OS mediating fertility in a male plant.
XX
XX PN Claim 4; Page 46; 50pp; English.
XX
XX CC The invention provides a male tissue-preferred regulatory region (I)
XX
XX CC comprising nucleotide sequences essential for initiating transcription of
XX
XX CC the Ms45 gene. A method of mediating male fertility in a plant is
XX
XX CC provided that involves introducing an expression vector comprising a
XX
XX CC promoter operably linked to (I) into a plant where the exogenous gene
XX
XX CC impacts male fertility of the plant and (I) controls expression of the
XX
XX CC exogenous gene. A method of producing hybrid seeds is also provided. The
XX
XX CC present sequence represents a nucleic acid sequence encoding an Ms45 male
XX
XX CC -tissue preferred regulatory region from Z. mays
XX
XX SQ Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 40; DB 5; Length 1394;
XX
XX Best Local Similarity 100.0%; Pred. No. 6.8e-06;
XX
XX Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
XX
XX DB 1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278
XX
XX
XX RESULT 8
AAH76333
ID AAH76333 standard; DNA; 1394 BP.
XX
XX AC AAH76333;
XX
XX XX 29-OCT-2001 (first entry)
XX
XX DE Z. mays Ms45 male tissue-preferred regulatory region encoding DNA.
XX
XX KW Ms45; male tissue; regulatory region; transcription; male fertility;
XX
XX KW hybrid seed; ds.
XX
XX OS Zea mays.
XX
XX PN WO200160997-A2.

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XX
XX PD 23-AUG-2001.
XX
XX PF 13-FEB-2001; 2001WO-US004527.
XX
XX PR 15-FEB-2000; 2000US-00504487.
XX
XX PA (PION-) PIONEER HI-BRED INT INC.
XX
XX PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
XX
XX DR WPI; 2001-514772/56.
XX
XX PT A male tissue-preferred regulatory region comprising nucleotide sequences
XX
XX KW essential for initiating transcription of the Ms45 gene useful for
XX
XX OS mediating fertility in a male plant.
XX
XX PN Claim 4; Page 47; 50pp; English.
XX
XX CC The invention provides a male tissue-preferred regulatory region (I)
XX
XX CC comprising nucleotide sequences essential for initiating transcription of
XX
XX CC the Ms45 gene. A method of mediating male fertility in a plant is
XX
XX CC provided that involves introducing an expression vector comprising a
XX
XX CC promoter operably linked to (I) into a plant where the exogenous gene
XX
XX CC impacts male fertility of the plant and (I) controls expression of the
XX
XX CC exogenous gene. A method of producing hybrid seeds is also provided. The
XX
XX CC present sequence represents a nucleic acid sequence encoding an Ms45 male
XX
XX CC -tissue preferred regulatory region from Z. mays
XX
XX SQ Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 40; DB 5; Length 1394;
XX
XX Best Local Similarity 100.0%; Pred. No. 6.8e-06;
XX
XX Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
XX
XX DB 1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278
XX
XX
XX RESULT 9
ACL38730
ID ACL38730 standard; cDNA; 2000 BP.
XX
XX AC ACL38730;
XX
XX DT 02-JUN-2005 (first entry)
XX
XX DE Rice stress-regulated promoter SEQ ID NO:17293.
XX
XX KW ss; abiotic stress tolerance; transgenic plant; plant; cereal;
XX
XX KW agriculture.
XX
XX OS Oryza sativa.
XX
XX PN WO2003008540-A2.
XX
XX PD 30-JAN-2003.
XX
XX PF 21-JUN-2002; 2002WO-US019668.
XX
XX PR 22-JUN-2001; 2001US-0300112P.
XX
XX PR 24-AUG-2001; 2001US-0314662P.
XX
XX PR 26-SEP-2001; 2001US-0325277P.
XX
XX PR 21-NOV-2001; 2001US-0332132P.
XX
XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX PI Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
XX
XX PI Moughamer T, Provart N, Rickes D, Zhu T;
XX
XX DR WPI; 2003-248011/24.

```

PT New stress-responsive nucleic acid, useful for altering the
 PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
 PT stress, salt stress or osmotic stress.

XX Claim 48; SEQ ID NO 17293; 89pp; English.

CC The invention relates to novel abiotic stress responsive polynucleotides
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host
 CC cells, and plants containing such polynucleotides. Also disclosed are
 CC methods for using the polynucleotides and polypeptides to alter the
 CC responsiveness of a plant to abiotic stress. The invention is useful in
 CC agriculture. The nucleic acid is useful for determining whether a test
 CC plant has been exposed to an abiotic stress condition. It is also useful
 CC for selecting an agent that alters abiotic stress regulated
 CC polynucleotide expression in a plant cell, and to identify a homolog or
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
 CC molecule and the polypeptide encoded by it are useful in altering the
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
 CC stress, osmotic stress or any of their combinations. The present sequence
 CC is used in the exemplification of the invention

XX Sequence 2000 BP; 616 A; 370 C; 355 G; 659 T; 0 U; 0 Other;

Query Match 76.0%; Score 30.4; DB 11; Length 2000;
 Best Local Similarity 85.0%; Pred. No. 0.047;
 Matches 34; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAAC 40
 DB 1840 AGAACACCTACTCCCAACAAATCCATCTTACTCATGCAAC 1879

RESULT 10

ACN45146
 ID ACN45146 standard; DNA; 226215 BP.

XX ACN45146;

XX 18-NOV-2004 (first entry)

XX Human genomic sequence HCG1639824.

XX Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.

XX Homo sapiens.

XX WO2003073826-A2.

XX 12-SEP-2003.

XX 28-FEB-2003; 2003WO-US006235.

XX 01-MAR-2002; 2002US-00087192.

XX (SAGR-) SAGRES DISCOVERY.

XX Morris DW;

XX WPI; 2003-328604/31.

XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
 PT comprises a nucleotide sequence.

XX Claim 1; SEQ ID NO 1948; Opp; English.

CC The present invention relates to novel DNA and protein sequences which
 CC are associated with carcinomas. The sequences are useful for: (i) for
 CC screening drug candidates; (ii) for screening of bioactive agent capable
 CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
 CC a bioactive agent capable of modulating the activity of CAP; (iv) for
 CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
 CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
 CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;

CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
 CC determining Carcinoma Associated (CA) gene copy number. In addition, the
 CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
 CC carcinoma including lymphoma. The present sequence is one such CA coding
 CC sequence. Note: This patent is an equivalent to basic patent
 CC US2002182586A1, for which no sequence data was published

XX Sequence 226215 BP; 65331 A; 42804 C; 45218 G; 72862 T; 0 U; 0 Other;

Query Match 56.0%; Score 22.4; DB 11; Length 226215;

Best Local Similarity 72.5%; Pred. No. 1.4e+02;

Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAAC 40

DB 183206 AGAATTCCTGCTCCAAACACAGCATCTTACTCCTTTTAC 183245

RESULT 11

ABZ10202/C

ID ABZ10202 standard; DNA; 4110 BP.

XX ABZ10202;

XX 16-JAN-2003 (first entry)

XX Haematopoietic cell proliferation disorder related DNA sequence #342.

XX Human; haematopoietic cell proliferation disorder; cytostatic;

XX gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;

XX cytosine methylation state; gene; ds.

XX Homo sapiens.

XX WO200277272-A2.

XX 03-OCT-2002.

XX 26-MAR-2002; 2002WO-EP003401.

XX 26-MAR-2001; 2001US-0278333P.

XX (EPIG-) EPIGENOMICS AG.

XX Berlin K.; Braum A.; Distler J.; Guetig D.; Howe A.; Mueller J.;

XX Olek A.; Piepenbrock C.; Adorjan P.; Grabs G.; Lesche R.; Leu E.;

XX Lewin A.; Lippecher E.; Maier S.; Model F.; Mueller V.; Otto T.; Pelet C.;

XX Schwope I.; Ziebarth H.;

XX WPI; 2003-018942/01.

XX Detecting and differentiating between hematopoietic cell proliferative
 PT disorders, comprises contacting a target nucleic acid with a reagent that
 PT distinguishes between methylated and non-methylated CpG dinucleotides.

XX Claim 28; SEQ ID NO 342; 117pp; English.

CC The present invention describes a method for detecting and
 CC differentiating between haematopoietic cell proliferative disorders
 CC associated with at least 1 gene and/or their regulatory regions in a
 CC subject. The method comprises contacting a target nucleic acid in a
 CC biological sample obtained from the subject with at least 1 reagent,
 CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
 CC represent specifically claimed nucleotide sequences from the present
 CC invention. Oligonucleotides from the present invention can be used for
 CC differentiating between healthy haematopoietic cells and proliferative
 CC lymphocytic leukaemia and acute myelogenous leukaemia, as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of haematopoietic cell proliferation disorder related DNA

CC sequences. The nucleotide sequences from the present invention can also
 CC be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC haematopoietic cell proliferative disorders. The present method enables a
 CC highly specific classification of haematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients

XX SQ Sequence 4110 BP; 945 A; 0 C; 1132 G; 2033 T; 0 U; 0 Other;

Query Match 54.0%; Score 21.6; DB 8; Length 4110;
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ATACCTACTCCCAACCAATCCATCTTAC 31
 Db 3083 AACCTAACCCCAACCAATCCATCTTAC 3056

RESULT 12

ABL32304/C
 ID ABL32304 standard; DNA; 6309 BP.

XX AC ABL32304;

XX DT 26-MAR-2002 (first entry)

XX DE Human immune system associated gene SEQ ID NO: 277.

XX KW Human; immune system disease; cytosine methylation; antiasthmatic;
 KW antiarteriosclerotic; antianemic; cytostatic; nootropic;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 KW antirheumatic; antarthritic; antidiabetic; antipeoriatic;
 KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
 XX ds.

XX OS Homo sapiens.

XX FN WO200200928-A2.

XX PD 03-JAN-2002.

XX PF 02-JUL-2001; 2001WO-EP007537.

XX PR 30-JUN-2000; 2000DE-01032529.

XX PR 01-SEP-2000; 2000DE-01043826.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2002-130909/17.

XX PT Nucleic acid comprising fragment of chemically modified gene, useful for
 PT diagnosis and treatment of diseases associated with abnormal cytosine
 PT methylation.

XX PS Claim 1; SEQ ID NO 277; 32pp + Sequence Listing; German.

XX CC The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention

XX SQ Sequence 6309 BP; 1758 A; 69 C; 1364 G; 3118 T; 0 U; 0 Other;

Query Match 54.0%; Score 21.6; DB 6; Length 6309;

Best Local Similarity 75.0%; Pred. No. 1.7e+02;

Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 4 ATACCTACTCCCAACCAATCCATCTTAC 39
 Db 3335 ATACCTATTTCCTATAGACCAATCTCAATAATCCAA 3300

RESULT 13

ADB54282/C
 ID ADB54282 standard; DNA; 7110 BP.

XX AC ADB54282;

XX DT 04-DEC-2003 (first entry)

XX DE Pretreated genomic DNA region 206.

XX KW colon cell proliferative disorder; non methylated CpG dinucleotide;
 KW cytostatic; cancer; adenoma; carcinoma; cytosine methylation state; ds.
 XX Unidentified.

XX PN WO2003072821-A2.

XX PD 04-SEP-2003.

XX PF 27-FEB-2003; 2003WO-EP002035.

XX PR 27-FEB-2002; 2002EP-00004551.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Adorjan P, Burger M, Maier S, Nimmrich I, Becker E, Lesche R;
 XX Rujan T, Schmitt A;

XX DR WPI; 2003-731620/69.

XX PT Detecting and differentiating between colon cell proliferative disorders
 XX associated with a gene or its regulatory regions comprises contacting a
 XX target nucleic acid in a biological sample obtained from the subject with
 XX a reagent.

XX PS Claim 32; SEQ ID NO 338; 74pp; English.

XX CC The invention relates to a novel method for detecting and differentiating
 XX between colon cell proliferative disorders associated with at least one
 XX gene or its regulatory regions. The method comprises contacting a target
 XX nucleic acid in a biological sample obtained from the subject with at
 XX least one reagent or a series of reagents, where the reagent or series of
 XX reagents distinguishes between methylated and non methylated CpG
 XX dinucleotides within the target nucleic acid. The molecules of the
 XX invention demonstrate cytosine methylation activity whilst the method may useful
 XX for detecting and differentiating between colon cell proliferative
 XX disorders, including cancers such as colon adenoma and colon carcinoma.
 XX The PNA (peptide nucleic acid)-oligomers are useful as probes for
 XX determining cytosine methylation state or single nucleotide
 XX polymorphisms. The current sequence is that of the pretreated genomic DNA
 XX region of the invention. This sequence is not shown within the
 XX specification but is taken from Wipoweb.

XX SQ Sequence 7110 BP; 1818 A; 0 C; 1721 G; 3571 T; 0 U; 0 Other;

Query Match 54.0%; Score 21.6; DB 10; Length 7110;

Best Local Similarity 85.7%; Pred. No. 1.7e+02;

Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ATACCTACTCCCAACCAATCCATCTTAC 31

Db 3083 AACCTAACCCCAACCAATCCATCTTAC 3056

RESULT 14

ADE84196/C

ID ADE84196 standard; DNA; 7110 BP.
XX ADE84196;
AC
XX
DT 29-JAN-2004 (first entry)
XX
DE Human lymphoid cell proliferative disorder gene derived DNA #132.
XX
XX ds; lymphoid cell proliferative disorder; methylation;
KW methylated CpG dinucleotide; single nucleotide polymorphism; SNP;
KW diffuse large B-cell lymphoma; mantle cell lymphoma;
KW chronic lymphocytic leukemia; small lymphocytic lymphoma;
KW follicular lymphoma; diagnosis; prognosis.
XX
XX Homo sapiens.
XX
XX WO2003044226-A2.
XX
XX 30-MAY-2003.
XX
XX 25-NOV-2002; 2002WO-EP013265.
XX
XX 23-NOV-2001; 2001DE-01057491.
XX
XX 28-DEC-2001; 2001DE-01064501.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimmrich I;
XX
XX WPI; 2003-457621/43.
XX
XX Detecting and differentiating between lymphoid cell proliferative
PT disorders comprising a target nucleic acid with at least one
PT reagent that distinguishes between methylated and non-methylated CpG
PT dinucleotides.
XX
XX Claim 26; SEQ ID NO 192; 448pp; English.
XX
XX The invention relates to a method of detecting and differentiating
CC between lymphoid cell proliferative disorders associated with at least
CC one gene and/or their regulatory regions in a subject by contacting a
CC target nucleic acid in a biological sample obtained from the subject with
CC at least one reagent or series of reagents that distinguish between
CC methylated and non-methylated CpG dinucleotides within the target nucleic
CC acid. The genes and/or their regulatory regions are preferably selected
CC from MDR1, CSNK2B, EGR4, AR, CDK4, RB2, CDC25A, GIPB beta, MYO11, CDH3,
CC MYCL1, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN2A, CDKN2B, FOS,
CC GSTP1, HIC-1, MGMT, MLH1, MDS, MYC, PTEN, RBL2, TGFBR2, TP73, CDKN1C,
CC GSK3beta, ESRI, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic
CC acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences
CC of the genes are useful for detecting the methylation state of all the
CC CpG dinucleotides within one or more the sequences, or their complements,
CC for determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) and for differentiating at least two of the medical
CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,
CC chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular
CC lymphoma. They are also useful for detecting or a predisposition to,
CC differentiation between subclasses, diagnosis, prognosis, treating and/or
CC monitoring of lymphoid cell proliferative disorder. This sequence
CC represents a nucleic acid of a pretreated genomic DNA derived from the
CC above mentioned genes.
XX
XX Sequence 7110 BP; 1818 A; 0 C; 1721 G; 3571 T; 0 U; 0 Other;
SQ

Query Match 54.0%; Score 21.6; DB 10; Length 7110;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps .0;
QY 4 ATACCTACTCCCAACATCCATCTTAC 31
DB 3083 AACCTTACCCCAACATCCATCTTAC 3056

RESULT 15
ADS9580/c
ID ADS9580 standard; DNA; 7110 BP.
XX
AC ADS9580;
XX
DT 18-NOV-2004 (first entry)
XX
DE Oligonucleotide of the invention SEQ ID NO:596.
XX
XX ss; cell proliferative disorder; breast; methylation; cytostatic;
KW gene therapy; single nucleotide polymorphism; SNP.
KW
XX OS Unidentified.
XX
XX WO2004035803-A2.
XX
XX 29-APR-2004.
XX
XX 01-OCT-2003; 2003WO-EP010881.
XX
XX 01-OCT-2002; 2002DE-01045779.
XX
XX 07-JAN-2003; 2003DE-01000096.
XX
XX 17-APR-2003; 2003DE-01017955.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Poekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;
XX Nimmrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;
XX
XX WPI; 2004-348468/32.
XX
XX Predicting responsiveness of a subject with breast cell proliferative
PT disorder, useful for treating or differentiating breast cell
PT proliferative disorders comprises analyzing methylation pattern of a
PT genomic DNA from the subject.
XX
XX Disclosure; SEQ ID NO 596; 104pp; English.
XX
XX The invention relates to a novel method for predicting the responsiveness
CC of a subject with a cell proliferative disorder of the breast tissues to
CC a therapy comprising analyzing the methylation pattern of a target
CC nucleic acid by contacting at least one of the target nucleic acids in a
CC biological sample obtained from the subject prior to or during treatment.
CC The method of the invention has cytostatic activity, and may have a use
CC in gene therapy. The set of oligonucleotides comprising at least two of
CC the oligomers are useful for detecting the cytosine methylation state of
CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The
CC methods, nucleic acid, oligonucleotide, and kit are useful for the
CC treatment, characterization, classification and/or differentiation, of
CC breast cell proliferative disorders. The method is also useful for
CC predicting the responsiveness of a subject with a cell proliferative
CC disorder of the breast tissues to a therapy. The present sequence is used
CC in the exemplification of the invention.
XX
XX Sequence 7110 BP; 1818 A; 0 C; 1721 G; 3571 T; 0 U; 0 Other;
SQ

Query Match 54.0%; Score 21.6; DB 13; Length 7110;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 ATACCTACTCCCAACATCCATCTTAC 31
DB 3083 AACCTTACCCCAACATCCATCTTAC 3056

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Job time : 28.619 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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(without alignments)
9910.279 Million cell updates/sec

Title: US-10-713-381-1_COPY_1239_1278

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_hic:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_est8:
10: gb_est9:
11: gb_est10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	40	100.0	687	9	CC656939
2	40	100.0	915	10	CG224225
3	40	100.0	963	9	CC656933
4	35.2	88.0	702	10	CW324514
5	24.2	60.5	528	8	CW445575
6	23.8	59.5	528	8	H24137
7	23.6	59.0	375	9	B2705605
8	23.2	58.0	738	11	CR181951
9	23.2	58.0	703	11	CR181951
10	23.2	58.0	1018	10	CL109241
11	23.2	58.0	1253	6	CD495749
12	23	57.5	405	9	A2883408
13	23	57.5	662	7	CJ037346
14	23	57.5	790	7	CJ035837
15	23	57.5	798	2	BG506830
16	23	57.5	968	2	BF143726
17	22.8	57.0	771	3	BM406466
18	22.8	57.0	1044	8	DN570622
19	22.6	56.5	398	10	CW888409
20	22.6	56.5	410	1	AW257178
21	22.6	56.5	560	2	BE205271
22	22.6	56.5	624	11	CR843833

C 23	22.6	56.5	630	9	BZ173201
C 24	22.6	56.5	644	11	CR843905
C 25	22.6	56.5	664	9	AZ400686
C 26	22.6	56.5	691	1	AW687128
C 27	22.6	56.5	736	11	CR818130
C 28	22.6	56.5	1080	10	CL058859
C 29	22.4	56.0	298	2	BB264116
C 30	22.4	56.0	804	8	DT054853
C 31	22.4	56.0	940	7	CK864514
C 32	22.4	56.0	940	7	CK871857
C 33	22.4	56.0	951	7	CN317130
C 34	22.2	55.5	273	1	AI206216
C 35	22.2	55.5	346	1	AI598201
C 36	22.2	55.5	398	1	AI725064
C 37	22.2	55.5	417	1	AI467879
C 38	22.2	55.5	479	2	BF601210
C 39	22.2	55.5	491	1	AI382034
C 40	22.2	55.5	609	3	BM027586
C 41	22.2	55.5	727	7	CK949745
C 42	22.2	55.5	802	10	CG811817
C 43	22.2	55.5	874	10	CZ727957
C 44	22.2	55.5	940	10	CG383910
C 45	22.2	55.5	1090	10	CL084441

ALIGNMENTS

RESULT 1
CC656939/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
ORIGIN

CC656939
OGWDQ20TV_ZM_0.7-1.5-KB Zea mays genomic clone ZMMBma0554D15,
genomic survey sequence.
CC656939
CC656939.1 GI:32060231
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 687)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Renick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGWDQ20TM
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.
Location/Qualifiers
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/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBma0554D15"
/note="Vector: pBCSK; Site 1, HincII: 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 100.0%; Score 40; DB 9; Length 687;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 40; Conservative 0; Indels 0; Gaps 0;
QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40

```

|||||
337 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAAC 298

RESULT 2
CG224225          915 bp   DNA       linear   GSS 22-AUG-2003
LOCUS              OGIAG08TV_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZMMBMA0716B15,
DEFINITION          genomic survey sequence.
ACCESSION           CG224225
VERSION             CG224225.1  GI:34124113
KEYWORDS            GSS.
SOURCE              Zea mays
ORGANISM            Zea mays
                    /organism="Zea mays"
                    /mol_type="genomic DNA"
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                    /clone_lib="ZMMBMA0554D15"
                    /clone_lib="ZM_0.7_1.5_KB"
REFERENCE           1 (bases 1 to 915)
AUTHORS             Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
                    Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
TITLE               Consortium for Maize Genomics
JOURNAL             Unpublished (2002)
COMMENT             Other_GSSs: OGIAG08TH
                    Contact: Cathy Whitelaw
                    TIGR
                    9712 Medical Center Drive, Rockville, MD 20850, USA
                    Tel: 301-838-5843
                    Fax: 301-838-0208
                    Email: whitelaw@tigr.org
                    Seq primer: TP
                    Class: methylation filtered.
                    Location/Qualifiers
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                        methylation filtered genomic DNA library"

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Query Match      100.0%; Score 40; DB 10; Length 915;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAAC 40
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Db 618 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAAC 657

RESULT 3
CG656933          963 bp   DNA       linear   GSS 19-JUN-2003
LOCUS              OGWDQ20TM_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZMMBMA0554D15,
DEFINITION          genomic survey sequence.
ACCESSION           CG656933
VERSION             CG656933.1  GI:32060225
KEYWORDS            GSS.
SOURCE              Zea mays
ORGANISM            Zea mays
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                    /mol_type="genomic DNA"
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                    methylation filtered genomic DNA library"

ORIGIN
Query Match      100.0%; Score 40; DB 10; Length 915;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAAC 40
    |||||
Db 618 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAAC 657

RESULT 3
CG656933          963 bp   DNA       linear   GSS 19-JUN-2003
LOCUS              OGWDQ20TM_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZMMBMA0554D15,
DEFINITION          genomic survey sequence.
ACCESSION           CG656933
VERSION             CG656933.1  GI:32060225
KEYWORDS            GSS.
SOURCE              Zea mays
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                    /clone_lib="ZM_0.7_1.5_KB"
                    /note="Vector: pBCSK(-); Site 1: HincII; DNA
                    prepared from purified nuclei was randomly sheared,

CONTACT: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
Location/Qualifiers
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FEATURES
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    /note="Vector: pBCSK(-); Site 1: HincII; 0.7-1.5 kb
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ORIGIN
Query Match      100.0%; Score 40; DB 9; Length 963;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAAC 40
    |||||
Db 836 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAAC 875

RESULT 4
CW324514          702 bp   DNA       linear   GSS 31-OCT-2004
LOCUS              104819_11477203_148_35910_078 Sorghum_methylation_filtered_library
DEFINITION          (LibID: 104) Sorghum bicolor genomic clone 11477203, genomic survey
                    sequence.
ACCESSION           CW324514
VERSION             CW324514.1  GI:55040702
KEYWORDS            GSS.
SOURCE              Sorghum bicolor (sorghum)
ORGANISM            Sorghum bicolor
                    /organism="Sorghum bicolor"
                    /mol_type="genomic DNA"
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                    methylation filtered genomic DNA library"

REFERENCE           1 (bases 1 to 702)
AUTHORS             Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
                    Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
                    McMenamy,J., Smith,M., Holman,H., Roe,B.A., Wiley,G., Korf,I.F.,
                    Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddelloh,J.A. and
                    Martienssen,R.A.
TITLE               Sorghum genome sequencing by methylation filtration
JOURNAL             PLoS Biol. 3 (1), e13 (2005)
PUBLISHED           15660154
COMMENT             Contact: Bedell JA
                    Orion Genomics, LLC
                    4041 Forest Park Ave, St. Louis, MO 63108, USA
                    Tel: 314 615 6979
                    Fax: 314 615 5975
                    Email: jbedell@oriongenomics.com
                    Plate: 819 row: c column: 19
                    Seq primer: SWfor Forward
                    Class: methylation filtered
                    High quality sequence stop: 702.
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                        104)"
                        /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
                        prepared from purified nuclei was randomly sheared,

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end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

ORIGIN

Query Match 88.0%; Score 35.2; DB 10; Length 702;
Best Local Similarity 92.5%; Pred. No. 0.0034; 3; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 0; Gaps 0;

OY 1 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAAC 40
|||||
DB 74 AGGACACCTACTCCCAACAAATCCATGTTACCCATGCAAC 113
|||||

RESULT 5
CW445575 296 bp DNA linear GSS 02-NOV-2004
LOCUS fbb001f170m16k0 Sorghum methylation filtered library (LibID: 104)
DEFINITION Sorghum bicolor genomic clone fbb001f170m16, genomic survey
sequence.

ACCESSION

CW445575

VERSION

GSS

KEYWORDS

Sorghum bicolor (sorghum)

SOURCE

Sorghum bicolor

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD

clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 296)

Bedell, J.A., Budiman, M.A., Nurnberg, A., Citek, R.W., Robbins, D.,

Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,

McMenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korf, I.F.,

Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddell, J.A. and

Martensen, R.A.

Sorghum genome sequencing by methylation filtration

PLoS Biol. 3 (1); e13 (2005)

15660154

Contact: Bedell JA

Orion Genomics, LLC

4041 Forest Park Ave, St. Louis, MO 63108, USA

Tel: 314 615 6979

Fax: 314 615 5975

Email: jbedell@oriongenomics.com

Plate: fbb001f170 row: m column: 16

Seq primer: k Reverse

Class: methylation filtered

High quality sequence stop: 296.

Location/Qualifiers

1..296

/organism="Sorghum bicolor"

/mol_type="genomic DNA"

/cultivar="ATx623"

/db_xref="taxon:4558"

/clone="fbb001f170m16"

/clone_lib="Sorghum methylation filtered library (LibID: 104)"

/note="Organ: leaf; Vector: pBCSK(-); Site: 1; HincII; DNA prepared from purified nuclei was randomly sheared end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

RESULT 6
H24137 528 bp mRNA linear EST 06-JUL-1995
LOCUS YMS0G08.r1 Soares infant brain INIB Homo sapiens cDNA clone
DEFINITION IMAGE:51939 5', mRNA sequence.

ACCESSION H24137

VERSION H24137.1

KEYWORDS GI:892832

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 528)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and

Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estw@wustl.edu

Insert Size: 1161

High quality sequence stops: 349

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1161

Seq primer: M13RP1

High quality sequence stop: 349.

Location/Qualifiers

1..528

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:424875"

/db_xref="taxon:9606"

/clone="IMAGE:51939"

/sex="female"

/dev_stage="73 days post natal"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares infant brain LNLB"

/note="Organ: whole brain; Vector: Lfamid BA; Site: 1; Not

1; Site 2: Hind III; 1st strand cDNA was primed with a Not

1 - oligo(dT) primer [5'

AACTCGAAGAAATTCGCGCGCAGGAATTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Hind III adaptors

(Pharmacia), digested with Not I and directionally cloned

into the Not I and Hind III sites of the Lfamid BA vector.

Library went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

0;

59.5%;

Score 23.8;

DB 8;

Length 528;

Pred. No. 1.2e+02;

0;

0;

0;

0;

0;

0;

0;

OY

4 ATACTCTCTCCCAACAAATCCATCTTACTCATGCA 38

|||||

DB 346 AAATCTACTCTCAACAAATTCATCTTATACATGCA 380

|||||

RESULT 7

BZ706605/c

LOCUS

DEFINITION

BZ706605

SM416B1-G07 55 13.ab1 Spider Monkey genomic BAC library Ateles

geoffroyi genomic, genomic survey sequence.

375 bp

DNA

linear

GSS 18-MAY-2003

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

1;

60.5%;

Score 24.2;

DB 10;

Length 296;

Pred. No. 75;

37; Conservative

0; Mismatches

3; Indels

1; Gaps

1;

1;

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SOURCE
ORGANISM
Xenopus tropicalis (western clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Silurana
1 (bases 1 to 1018)
Kremetzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E., and Wilson, R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: Sp6 ATTGAGTGCACACTATAG
Class: BAC ends
High quality sequence start: 72
High quality sequence stop: 524.
Location/Qualifiers
1..1018
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db_xref="taxon:8364"
/clone_lib="ISB1-51D14"
/note="Vector: pBelobAC11; ISB-1 Xenopus tropicalis BAC
Library Segment 1"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source
1..1253
/organism="Gasterosteus aculeatus"
/mol_type="mRNA"
/strain="Salinas river, CA"

ORIGIN
Query Match 58.0%; Score 23.2; DB 10; Length 1018;
Best Local Similarity 77.8%; Pred. No. 2.3e+02;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 5 TACCTACTCCCAACATCCATCTTACTCATGCAAC 40
DB 156 TACCTACTCCCAACATCCATCTTACTCATGCAAC 121

RESULT 11
CD495749 1253 bp mRNA linear EST 12-JUN-2003
LOCUS CD418-D05.yid-s SHGC-CDA Gasterosteus aculeatus cDNA clone
DEFINITION CD418-D05 3', mRNA sequence.
ACCESSION CD495749.1 GI:31422780
VERSION CD495749
KEYWORDS EST.
SOURCE Gasterosteus aculeatus (three spined stickleback)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
Gasterosteidae; Gasterosteus.
1 (bases 1 to 1253)
Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M.,
Schmutz, J., and Myers, R.M.
Expressed sequence tags from Gasterosteus aculeatus
Unpublished (2003)
Contact: Kingsley, DW
HHMI and Department of Developmental Biology
Stanford University School of Medicine
Beckman Center B300, 279 Campus Drive, Stanford, CA 94305-5329, USA
Tel: 650 725 5954
Fax: 650 725 7739
Email: kingsley@cngm.stanford.edu
Plate: 18
High quality sequence start: 15
High quality sequence stop: 667.
Location/Qualifiers
1..1253
/organism="Gasterosteus aculeatus"
/mol_type="mRNA"
/strain="Salinas river, CA"

ORIGIN
Query Match 58.0%; Score 23.2; DB 6; Length 1253;
Best Local Similarity 77.8%; Pred. No. 2.4e+02;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 5 TACCTACTCCCAACATCCATCTTACTCATGCAAC 40
DB 1047 TACCTACTCCCAACATCCATCTTACTCATGCAAC 1082

RESULT 12
AZ883408 405 bp DNA linear GSS 05-MAR-2001
LOCUS RPCI-23-189L2.TJ RPCI-23 Mus musculus genomic clone RPCI-23-189L2,
DEFINITION genomic survey sequence.
ACCESSION AZ883408
VERSION AZ883408.1 GI:13202353
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 405)
Zhao, S., Niernan, W., Feldblyum, T., Malek, J., Shatsman, S.,
Akin, B., B. Levins, M., McGann, S., Teagay, G., Geer, K., Krol, M., de
Jong, F., and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-189L2.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 189 row: L column: 2
Seq primer: SP6
Class: BAC ends
Location/Qualifiers
1..405
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-189L2"

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/sex="Female"
/lab host="DH10B"
/clone_lib="RPCI-23"
/notes="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
ECORI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI MethyIase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
ORIGIN
Query Match          57.5%; Score 23; DB 9; Length 405;
Best Local Similarity 74.4%; Pred. No. 2.4e+02;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 1 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAA 39
Db 182 AGGTAACAATAATCCCAACATGCTCTTCTAGTCATGCAA 144

RESULT 13
CJ037346
LOCUS
DEFINITION
CJ037346 662 bp mRNA linear EST 22-OCT-2004
scrofa cDNA clone TES01G080111 5', mRNA sequence.
ACCESSION
CJ037346
VERSION
CJ037346.1 GI:54561241
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE
1 (bases 1 to 662)
Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
Okumura,N., Hamasima,N. and Awata,T.
PEDE (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries
JOURNAL
Nucleic Acids Res. 32 (1), D484-D488 (2004)
PUBMED
14681463
COMMENT
Contact: Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library
Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.
FEATURES
source
1..662
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="TES01G080111"
/tissue_type="testis"
/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult
testis"
ORIGIN
Query Match          57.5%; Score 23; DB 7; Length 662;
Best Local Similarity 74.4%; Pred. No. 2.6e+02;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 1 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAA 39
Db 182 AGGTAACAATAATCCCAACATGCTCTTCTAGTCATGCAA 144

RESULT 13
CJ037346
LOCUS
DEFINITION
CJ037346 662 bp mRNA linear EST 22-OCT-2004
scrofa cDNA clone TES01G080111 5', mRNA sequence.
ACCESSION
CJ037346
VERSION
CJ037346.1 GI:54561241
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE
1 (bases 1 to 662)
Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
Okumura,N., Hamasima,N. and Awata,T.
PEDE (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries
JOURNAL
Nucleic Acids Res. 32 (1), D484-D488 (2004)
PUBMED
14681463
COMMENT
Contact: Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library
Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.
FEATURES
source
1..662
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="TES01G080111"
/tissue_type="testis"
/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult
testis"
ORIGIN
Query Match          57.5%; Score 23; DB 7; Length 662;
Best Local Similarity 74.4%; Pred. No. 2.6e+02;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 1 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAA 39
Db 182 AGGTAACAATAATCCCAACATGCTCTTCTAGTCATGCAA 144

```

```

|||||
611 AGGAACCTGACTCCCAACAACTAGTAAGTAATCTATCCAA 649
|||||

RESULT 14
CJ035837
LOCUS
DEFINITION
CJ035837 790 bp mRNA linear EST 22-OCT-2004
scrofa cDNA clone TES01E060090 5', mRNA sequence.
ACCESSION
CJ035837
VERSION
CJ035837.1 GI:54559732
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE
1 (bases 1 to 790)
Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
Okumura,N., Hamasima,N. and Awata,T.
PEDE (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries
JOURNAL
Nucleic Acids Res. 32 (1), D484-D488 (2004)
PUBMED
14681463
COMMENT
Contact: Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library
Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.
FEATURES
source
1..790
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="TES01E060090"
/tissue_type="testis"
/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult
testis"
ORIGIN
Query Match          57.5%; Score 23; DB 7; Length 790;
Best Local Similarity 74.4%; Pred. No. 2.7e+02;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 1 AGGATACCTACTCCCAACAACTAGTAAGTAATCTATCCAA 39
Db 609 AGGAACCTGACTCCCAACAACTAGTAAGTAATCTATCCAA 647
|||||

RESULT 15
BG506830/c
LOCUS
DEFINITION
BG506830 798 bp mRNA linear EST 27-MAR-2001
mRNA sequence.
ACCESSION
BG506830
VERSION
BG506830.1 GI:13468347
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

```

Wed Mar 8 14:17:01 2006

REFERENCE 1 (bases 1 to 798)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLC916 row: e column: 11
 High quality sequence stop: 2.
 Location/Qualifiers
 1..798
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4071154"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_77"
 /notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattagcc); Site 2: SfiI (ggccattagcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCGCATG-dr(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 57.5%; Score 23; DB 2; Length 798;
 Best Local Similarity 83.9%; Pred. No. 2.7e+02;
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 10 ACTCCCAACATCCATCTTACTCTGCAAC 40
 |||||
 DB 222 ACTCCCAACATCCATCTTACTCTGCAAC 192

Search completed: March 6, 2006, 01:57:48
 Job time : 191.843 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocollaboration Ltd.
OM nucleic - nucleic search, using sw model
Run on: March 5, 2006, 21:54:12 ; Search time 11.1834 Seconds
(without alignments)
6357.883 Million cell updates/sec
Title: US-10-713-381-1_COPY_1239_1278
Perfect score: 40
Sequence: 1 aggatcactctcccaacaatccttactctgcaac 40
Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0
Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Issued Patents NA:
1: /cgm2_6/prodata/1/ina/1 COMB.seq.*
2: /cgm2_6/prodata/1/ina/5 COMB.seq.*
3: /cgm2_6/prodata/1/ina/6A COMB.seq.*
4: /cgm2_6/prodata/1/ina/6B COMB.seq.*
5: /cgm2_6/prodata/1/ina/6 COMB.seq.*
6: /cgm2_6/prodata/1/ina/6CTUS COMB.seq.*
7: /cgm2_6/prodata/1/ina/6P COMB.seq.*
8: /cgm2_6/prodata/1/ina/6 RE COMB.seq.*
9: /cgm2_6/prodata/1/ina/backfiles1.seq.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				Description	
Result No.	Score	Query Match	Length DB ID		
1	40	100.0	1394	3	US-08-880-499-1
2	40	100.0	1394	3	US-08-880-499-2
C 3	20.6	51.5	601	3	US-09-949-002-7790
C 4	20.6	51.5	601	3	US-09-949-002-7791
5	20.6	51.5	1071	3	US-09-248-796A-5546
C 6	20.6	51.5	14882	3	US-09-949-002-782
C 7	20.6	51.5	42075	3	US-09-949-016-14995
C 8	20.4	51.0	601	3	US-09-949-016-65770
C 9	20.4	51.0	973	3	US-09-774-528-184
10	20.4	51.0	973	3	US-10-120-988-184
11	20.4	51.0	4201	3	US-08-945-056-4
C 12	20.4	51.0	51770	3	US-09-949-016-13668
C 13	20.4	51.0	84571	3	US-09-949-016-17420
C 14	20.4	51.0	126200	3	US-09-949-016-11824
C 15	20.4	51.0	126200	3	US-09-949-016-13193
C 16	20.2	50.5	5099	3	US-09-610-040-5
17	20.2	50.5	5099	3	US-10-267-763-5
18	20.2	50.0	601	3	US-09-949-016-88655
19	20.2	50.0	2615	3	US-09-620-312D-22
20	20.2	50.0	77586	3	US-09-949-016-13220
21	20.2	50.0	77586	3	US-09-949-016-13221
22	19.8	49.5	107	3	US-09-513-999C-19002
C 23	19.8	49.5	601	3	US-09-949-016-202698
C 24	19.8	49.5	1017	3	US-09-710-279-2867

C 25	19.8	49.5	1164	3	US-09-134-001C-2534
C 26	19.8	49.5	2046	3	US-09-248-796A-6906
C 27	19.8	49.5	2971	3	US-09-710-279-3449
C 28	19.8	49.5	9366	3	US-09-949-016-17437
C 29	19.8	49.5	74096	3	US-09-949-016-11785
C 30	19.8	49.5	74097	3	US-09-949-016-16239
C 31	19.8	49.5	265038	3	US-09-949-016-15779
C 32	19.6	49.0	189	3	US-09-540-236-1562
C 33	19.6	49.0	601	3	US-09-949-016-83110
C 34	19.6	49.0	601	3	US-09-949-016-83111
C 35	19.6	49.0	601	3	US-09-949-002-4265
C 36	19.6	49.0	964	3	US-09-775-398-26
C 37	19.6	49.0	4322	2	US-08-537-342-1
C 38	19.6	49.0	6330	3	US-09-949-016-15506
C 39	19.6	49.0	6886	3	US-09-596-002-29
C 40	19.6	49.0	75480	3	US-09-949-016-16090
C 41	19.6	49.0	80858	3	US-09-949-016-12659
C 42	19.6	49.0	80859	3	US-09-949-016-15715
C 43	19.6	49.0	89892	3	US-09-949-016-13667
C 44	19.6	49.0	107937	3	US-09-949-016-17192
C 45	19.6	49.0	140315	3	US-09-949-016-14141

ALIGNMENTS

RESULT 1
US-08-880-499-1
; Sequence 1, Application US/08880499
; Patent No. 6037523
; GENERAL INFORMATION:
; APPLICANT: Albertson, Marc C.
; APPLICANT: Fox, Tim W.
; APPLICANT: Carl, Garnaat W.
; APPLICANT: Hufman, Gary A.
; APPLICANT: Kendall, Timmy L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
; TITLE OF INVENTION: AND METHOD OF USING SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
; STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
; STREET: Box 1000
; CITY: Johnston
; STATE: Iowa
; COUNTRY: USA
; ZIP: 50131
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,499
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sweeney, Patricia A.
; REGISTRATION NUMBER: 32,733
; REFERENCE/DOCKET NUMBER: 0578
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800
; TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO. 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1394 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-880-499-1
Query Match 100.0%; Score 40; DB 3; Length 1394;

Best Local Similarity 100.0%; Pred. No. 6e-07; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 0;

Qy 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
|||||
Db 1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278
|||||

RESULT 2

US-08-880-499-2
; Sequence 2, Application US/08880499
; Patent No. 6037523
; GENERAL INFORMATION:
; APPLICANT: Albertson, Marc C.
; APPLICANT: Fox, Tim W.
; APPLICANT: Carl, Garmaat W.
; APPLICANT: Huffman, Gary A.
; APPLICANT: Kendall, Timmy L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
; TITLE OF INVENTION: AND METHOD OF USING SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
; STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
; STREET: Box 1000
; CITY: Johnston
; STATE: Iowa
; COUNTRY: USA
; ZIP: 50131
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,499
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sweeney, Patricia A.
; REGISTRATION NUMBER: 32,733
; REFERENCE/DOCKET NUMBER: 0578
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800
; TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1394 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-880-499-2

Query Match 100.0%; Score 40; DB 3; Length 1394;
Best Local Similarity 100.0%; Pred. No. 6e-07; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 0;

Qy 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
|||||
Db 1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278
|||||

RESULT 3

US-09-949-002-7790/c
; Sequence 7790, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790

; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7790
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-7790

Query Match 51.5%; Score 20.6; DB 3; Length 601;
Best Local Similarity 74.3%; Pred. No. 51;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 4 ATACCTACTCCCAACAATCCATCTTACTCATGCA 38
|||||
Db 496 ATAAAAACAACCAATCAATCAATCTTCTCATGCA 462
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RESULT 4

US-09-949-002-7791/c
; Sequence 7791, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7791
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-7791

Query Match 51.5%; Score 20.6; DB 3; Length 601;
Best Local Similarity 74.3%; Pred. No. 51;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 4 ATACCTACTCCCAACAATCCATCTTACTCATGCA 38
|||||
Db 379 ATAAAAACAACCAATCAATCAATCTTCTCATGCA 345
|||||

RESULT 5

US-09-248-796A-5546
; Sequence 5546, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 5546
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-5546

Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 2 GGATACCTACTCCCAACAAATCCATCTTACTCATGCAA 39
Db 626 GGAATCACTCCAAAGAAACCCCTCGAAACCATGCAA 663

RESULT 10

US-10-120-988-184
; Sequence 184, Application US/10120988

; Patent No. 6919193

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Goodrich, Ryle

; APPLICANT: Liu, Chenghua

; APPLICANT: Ren, Feiyan

; APPLICANT: Wang, Dunrui

; APPLICANT: Dwanac, Radoje T.

; TITLE OF INVENTION: No. 6919193el Nucleic Acids and

; TITLE OF INVENTION: Polypeptides

; FILE REFERENCE: 802CON

; CURRENT APPLICATION NUMBER: US/10/120,988

; CURRENT FILING DATE: 2002-04-11

; PRIOR APPLICATION NUMBER: 09/774,528

; PRIOR FILING DATE: 2001-01-30

; NUMBER OF SEQ ID NOS: 441

; SOFTWARE: pt_FL_genes version 2.0

; SEQ ID NO 184

; LENGTH: 973

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (231)..(749)

US-10-120-988-184

Query Match 51.0%; Score 20.4; DB 3; Length 973;

Best Local Similarity 71.1%; Pred. No. 68;

Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 2 GGATACCTACTCCCAACAAATCCATCTTACTCATGCAA 39
Db 626 GGAATCACTCCAAAGAAACCCCTCGAAACCATGCAA 663

RESULT 11

US-08-945-056-4

; Sequence 4, Application US/08945056

; Patent No. 607994

; GENERAL INFORMATION:

; APPLICANT: Coupland, George M.

; APPLICANT: Futterill, Joanna J.

; TITLE OF INVENTION: Genetic control of flowering

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Nixon & Vanderhye PC

; STREET: 8th Floor, 1100 No. 6077994th Glebe Road

; CITY: Arlington

; STATE: Virginia

; COUNTRY: United States of America

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/945,056

; FILING DATE: 20-OCT-1997

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB95/02561

; FILING DATE: 01-NOV-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9422083.7

; FILING DATE: 02-NOV-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Ms Mary J Wilson

; REGISTRATION NUMBER: 32,955

; REFERENCE/DOCKET NUMBER: 620-17

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4000

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4201 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ORIGINAL SOURCE:

; ORGANISM: Arabidopsis thaliana

; STRAIN: Landsberg erecta

; POSITION IN GENOME:

; MAP POSITION: chromosome 5

US-08-945-056-4

Query Match 51.0%; Score 20.4; DB 3; Length 4201;

Best Local Similarity 80.0%; Pred. No. 92;

Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GATACCTACTCCCAACAAATCCATCTTACT 32

Db 2631 GATACCAGCTCCACACCATCAAACTTACT 2660

RESULT 12

US-09-949-016-13668/c

; Sequence 13668, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13668

; LENGTH: 51770

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(51770)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-13668

Query Match 51.0%; Score 20.4; DB 3; Length 51770;

Best Local Similarity 71.1%; Pred. No. 1.6e+02;

Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 2 GGATACCTACTCCCAACAAATCCATCTTACTCATGCAA 39

Db 9851 GGATTCCTGGGCTCAAGCAATCCTCTGCTCAGGCAA 9814

RESULT 13

US-09-949-016-17420

; Sequence 17420, Application US/09949016

; Patent No. 6812339

US-09-949-016-11824/c
; Sequence 11824, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11824
; LENGTH: 84571
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(84571)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17420

Query Match 51.0%; Score 20.4; DB 3; Length 84571;
Best Local Similarity 71.1%; Pred. No. 1.7e+02;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 2 GGATCACTACTCCCAACATCCATCTTACTCTATGCAA 39
Db 24559 GGAATCAACTCCAAAGAACCTTCAAAACCATGCAA 24596

RESULT 14
US-09-949-016-11824/c
; Sequence 11824, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11824
; LENGTH: 126200
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(126200)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11824

Query Match 51.0%; Score 20.4; DB 3; Length 126200;
Best Local Similarity 71.1%; Pred. No. 1.9e+02;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 2 GGATCACTACTCCCAACATCCATCTTACTCTATGCAA 39
Db 53133 GGAATCAACTCCAAAGAACCTTCAAAATCATGCAA 53096

RESULT 15

US-09-949-016-13193/c
; Sequence 13193, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13193
; LENGTH: 126200
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(126200)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13193

Query Match 51.0%; Score 20.4; DB 3; Length 126200;
Best Local Similarity 71.1%; Pred. No. 1.9e+02;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 2 GGATCACTACTCCCAACATCCATCTTACTCTATGCAA 39
Db 53133 GGAATCAACTCCAAAGAACCTTCAAAATCATGCAA 53096

Search completed: March 5, 2006, 22:36:24
Job time : 13.1834 secs

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Sequence 231, Appl
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Sequence 24043, A
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Sequence 285327,
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Sequence 937247,
Sequence 20320, A
Sequence 2594, Ap
Sequence 361, App
Sequence 362, App
Sequence 198, App
Sequence 344, App
Sequence 1568, Ap

24 21.4 53.5 653 4 US-09-925-065A-63167
C 25 21.4 53.5 1341 3 US-09-938-842A-1555
C 26 21.4 53.5 1341 3 US-09-938-842A-1555
C 27 21.4 53.5 6681 6 US-10-311-455-128
C 28 21.4 53.5 6681 6 US-10-240-452-4
C 29 21.4 53.5 8168 6 US-10-311-455-901
C 30 21.4 53.5 8168 7 US-10-240-454-23
C 31 21.4 53.5 24401 10 US-11-097-143-2335
C 32 21.4 53.5 3673778 6 US-10-312-841-1
C 33 21.4 53.5 3673778 6 US-10-312-841-2
C 34 21.4 53.5 293 7 US-10-424-599-24043
C 35 21.4 53.5 617 4 US-09-925-065A-285326
C 36 21.4 53.5 617 4 US-09-925-065A-285327
C 37 21.4 53.5 653 4 US-09-925-065A-285328
C 38 21.4 53.5 653 4 US-09-925-065A-937247
C 39 21.4 53.5 931 7 US-10-424-599-20320
C 40 21.4 53.5 2000 7 US-10-260-238-2594
C 41 21.4 53.5 2792 7 US-10-041-018-361
C 42 21.4 53.5 3117 7 US-10-041-018-362
C 43 21.4 53.5 5507 8 US-10-473-126-198
C 44 21.4 53.5 5507 8 US-10-473-126-144
C 45 21.4 53.5 8404 6 US-10-311-455-1568

ALIGNMENTS

RESULT 1
US-10-713-381-6
; Sequence 6, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: USING SAME
; CURRENT APPLICATION NUMBER: US/10713381
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-6
Query Match 100.0%; Score 40; DB 8; Length 40;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGGATACCTCTCCCAACATCCATCTTACTCATGCAAC 40
DB 1 AGGATACCTCTCCCAACATCCATCTTACTCATGCAAC 40
RESULT 2
US-10-713-381-5
; Sequence 5, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: USING SAME

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Perfect score: 40
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0
Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084
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Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	40	100.0	50	US-10-713-381-5	Sequence 5, Appli
3	40	100.0	158	US-10-713-381-3	Sequence 3, Appli
4	40	100.0	255	US-10-713-381-9	Sequence 9, Appli
5	40	100.0	1394	US-10-713-381-1	Sequence 1, Appli
6	40	100.0	1394	US-10-713-381-2	Sequence 2, Appli
7	24	60.0	85779	US-10-713-381-6880	Sequence 6880, Ap
8	23.2	58.0	706	US-10-424-599-31006	Sequence 31006, A
9	23	57.5	636	US-09-925-065A-670302	Sequence 670302,
10	22.6	56.0	294	US-10-425-115-143168	Sequence 143168,
11	22.4	56.0	315	US-10-424-599-83179	Sequence 83179, A
12	22.4	56.0	226215	US-10-087-192-1948	Sequence 1948, Ap
13	22.2	55.5	611	US-09-925-065A-591011	Sequence 591011,
14	22.2	55.5	611	US-09-925-065A-591012	Sequence 591012,
15	22.2	55.5	611	US-09-925-065A-591013	Sequence 591013,
16	22.2	55.5	613	US-09-925-065A-253727	Sequence 253727,
17	22.2	55.0	628	US-09-925-065A-888321	Sequence 888321,
18	21.6	54.0	598	US-09-925-065A-393490	Sequence 393490,
19	21.6	54.0	4110	US-10-473-126-342	Sequence 342, App
20	21.6	54.0	6309	US-10-311-455-277	Sequence 277, App
21	21.4	53.5	560	US-09-925-065A-281837	Sequence 281837,
22	21.4	53.5	560	US-09-925-065A-281838	Sequence 281838,
23	21.4	53.5	620	US-09-925-065A-189248	Sequence 189248,

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; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-5

Query Match      100.0%; Score 40; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
   |||||
Db 11 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 50

RESULT 3
US-10-713-381-3
; Sequence 3, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 158
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-3

Query Match      100.0%; Score 40; DB 8; Length 158;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
   |||||
Db 86 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 125

RESULT 4
US-10-713-381-9
; Sequence 9, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
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; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-9

Query Match      100.0%; Score 40; DB 8; Length 255;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
   |||||
Db 99 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 138

RESULT 5
US-10-713-381-1
; Sequence 1, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-1

Query Match      100.0%; Score 40; DB 8; Length 1394;
Best Local Similarity 100.0%; Pred. No. 8e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
   |||||
Db 1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278

RESULT 6
US-10-713-381-2
; Sequence 2, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1394
; TYPE: DNA
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Db 1239 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 1278

Query Match 100.0%; Score 40; DB 8; Length 1394;
Best Local Similarity 100.0%; Pred. No. 8e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40

Db 1239 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 1278

RESULT 7

US-10-719-993-6880/c
; Sequence 6880, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 5342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6880
; LENGTH: 85779
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(85779)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-5)

Query Match 60.0%; Score 24; DB 8; Length 85779;
Best Local Similarity 84.4%; Pred. No. 47;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 ATACTTACTCCCAACATCCATCTTACTCAT 35

Db 16082 AAATTTACTCCCAACATCTTATGTCATCAT 16051

RESULT 8

US-10-424-599-31006
; Sequence 31006, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 31006
; LENGTH: 706
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_128002C.1

US-10-424-599-31006

Query Match 58.0%; Score 23.2; DB 7; Length 706;
Best Local Similarity 77.8%; Pred. No. 39;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 5 TACTTACTCCCAACATCCATCTTACTCATGCAAC 40

Db 455 TCCCTTCTCCCAACCTTCCATCACTCATACAAC 490

RESULT 9

US-09-925-065A-670302/c
; Sequence 670302, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 670302
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-925-065A-670302

Query Match 57.5%; Score 23; DB 4; Length 636;
Best Local Similarity 74.4%; Pred. No. 45;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 39

Db 474 AGGAACCGATTAACAAATATCCACCTTTCTCAGCAAC 436

RESULT 10

US-10-425-115-143168
; Sequence 143168, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 143168
; LENGTH: 294
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_62049C.1

US-10-425-115-143168

Query Match 56.5%; Score 22.6; DB 8; Length 294;
Best Local Similarity 86.2%; Pred. No. 56;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ATACTTACTCCCAACATCCATCTTACTCAT 32

Db 226 ATACTTGTGCTCCATACACTCCATCTTACT 254

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RESULT 11
US-10-424-599-83179
; Sequence 83179, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 83179
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_46127C.1
US-10-424-599-83179
Query Match 56.0%; Score 22.4; DB 7; Length 315;
Best Local Similarity 81.2%; Pred. No. 69;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4 ATACTACTCCCAACAATCCATCTTACTCAT 35
Db 211 AAACGACTCTTAACATCCATCTTAACTCT 242

RESULT 12
US-10-087-192-1948
; Sequence 1948, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 52945200122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1948
; LENGTH: 226215
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-1948
Query Match 56.0%; Score 22.4; DB 5; Length 226215;
Best Local Similarity 72.5%; Pred. No. 2,56+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 AGGATACCTATCCCAACAATCCATCTTACTCATGCAAC 40
Db 183206 AGAATTCCTGCTCCAAACACAGCATCTTACTCTTTTAC 183245

RESULT 13
US-09-925-065A-591011/c
; Sequence 591011, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 591012
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-591012
Query Match 55.5%; Score 22.2; DB 4; Length 611;
Best Local Similarity 88.9%; Pred. No. 94;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 14 CCAACAATCCATCTTACTCATGCAAC 40
Db 351 CCAACAACCAACCTTACTCATGCAGC 325

RESULT 14
US-09-925-065A-591012/c
; Sequence 591012, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 591012
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-591012
Query Match 55.5%; Score 22.2; DB 4; Length 611;
Best Local Similarity 88.9%; Pred. No. 94;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 14 CCAACAATCCATCTTACTCATGCAAC 40
Db 351 CCAACAACCAACCTTACTCATGCAGC 325

RESULT 15
US-09-925-065A-591013/c
; Sequence 591013, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
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US-10-713-381-1_copy_1239_1278.rnpbm

Wed Mar 8 14:17:00 2006

; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; CURRENT FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: US 60/243,096
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 60/252,147
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR APPLICATION NUMBER: US 60/250,092
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: US 60/261,766
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289,846
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 ; SEQ ID NO 591013
 ; LENGTH: 611
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-925-065A-591013

Query Match 55.5%; Score 22.2; DB 4; Length 611;
 Best Local Similarity 88.9%; Pred No. 94;
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 CCAAAACATCCATCTTACTCATCCAC 40
 Db 351 CCAAAACATCCATCTTACTCATCCAC 325

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 Job time : 59.5163 secs

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Wed Mar 8 14:17:00 2006

us-10-713-381-1_copy_1239_1278.rnpbn

Page 1

GenCore version 5.1.7
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Run on: March 6, 2006, 01:58:03 ; Search time 41.7555 Seconds
(without alignments)
2100.307 Million cell updates/sec

Title: US-10-713-381-1_COPY_1239_1278
Perfect score: 40
Sequence: 1 aggatactactcccaaacatccatcttactatgcac 40

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 14437070

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /csm2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
- 3: /csm2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
- 4: /csm2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
- 5: /csm2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
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- 9: /csm2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
- 10: /csm2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
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- 13: /csm2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	22.6	56.5	3242	8	US-10-750-185-58624
3	22.6	56.5	3242	8	US-10-750-185-58624
4	22.2	55.5	611	6	US-09-925-065A-591011
5	22.2	55.5	611	6	US-09-925-065A-591011
6	22.2	55.5	611	6	US-09-925-065A-591013
7	22.2	55.5	613	6	US-09-925-065A-253727
8	22	55.0	628	6	US-09-925-065A-888321
9	21.6	54.0	598	6	US-09-925-065A-393490
10	21.4	53.5	560	6	US-09-925-065A-281837
11	21.4	53.5	560	6	US-09-925-065A-281838
12	21.4	53.5	620	6	US-09-925-065A-189248
13	21.4	53.5	653	6	US-09-925-065A-63167
14	21	52.5	201	12	US-11-124-367A-24503
15	21	52.5	617	6	US-09-925-065A-285326
16	21	52.5	617	6	US-09-925-065A-285327
17	21	52.5	617	6	US-09-925-065A-285328
18	21	52.5	653	6	US-09-925-065A-937247
19	21	52.5	1718	8	US-10-750-185-62555
20	21	52.5	1718	8	US-10-750-623-62555

21	20.8	52.0	1109	8	US-10-750-185-49907
22	20.8	52.0	1109	8	US-10-750-623-49907
23	20.8	52.0	1217	8	US-10-750-185-57406
24	20.8	52.0	1217	8	US-10-750-623-57406
25	20.6	51.5	50	12	US-11-175-859-103341
26	20.6	51.5	569	6	US-09-925-065A-127036
27	20.6	51.5	586	6	US-09-925-065A-610819
28	20.6	51.5	664	6	US-09-925-065A-696032
29	20.6	51.5	664	6	US-09-925-065A-696033
30	20.4	51.0	201	8	US-10-995-561-70646
31	20.4	51.0	413	6	US-09-925-065A-360599
32	20.4	51.0	470	6	US-09-925-065A-951077
33	20.4	51.0	507	6	US-09-925-065A-589112
34	20.4	51.0	507	6	US-09-925-065A-589113
35	20.4	51.0	507	6	US-09-925-065A-166725
36	20.4	51.0	519	6	US-09-925-065A-241631
37	20.4	51.0	545	6	US-09-925-065A-785033
38	20.4	51.0	552	6	US-09-925-065A-659195
39	20.4	51.0	558	6	US-09-925-065A-910942
40	20.4	51.0	566	6	US-09-925-065A-104305
41	20.4	51.0	568	6	US-09-925-065A-573143
42	20.4	51.0	576	6	US-09-925-065A-575922
43	20.4	51.0	583	6	US-09-925-065A-575923
44	20.4	51.0	583	6	US-09-925-065A-575923
45	20.4	51.0	583	6	US-09-925-065A-575923

ALIGNMENTS

RESULT 1
US-09-925-065A-670302/c
Sequence 670302, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925.065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 670302
LENGTH: 636
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-670302

Query Match 57.5%; Score 23; DB 6; Length 636;
Best Local Similarity 74.4%; Pred. No. 11; Indels 0;
Matches 29; Conservative 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACATCCATCTTACTATGCAA 39
Db 474 AGGAACGGATTACCAACTATCCACCTTCTCAAGCAA 436

RESULT 2
US-10-750-185-58624
Sequence 58624, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:

```
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patent version 3.1
; SEQ ID NO 58624
; LENGTH: 3242
; TYPE: DNA
; ORGANISM: Bovine 19866880685452
US-10-750-185-58624

Query Match      56.5%; Score 22.6; DB 8; Length 3242;
Best Local Similarity 75.7%; Pred. No. 23;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy      4 ATACCTACTCCAAACAAATCCATCTTACTCATGCAAC 40
Db      2052 ATACCACCTACCAACCAAGTCAAGCTTATTGATGCAAC 2088

RESULT 3
US-10-750-623-58624
; Sequence 58624, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patent version 3.1
; SEQ ID NO 58624
; LENGTH: 3242
; TYPE: DNA
; ORGANISM: Bovine 19866880685452
US-10-750-623-58624

Query Match      56.5%; Score 22.6; DB 8; Length 3242;
Best Local Similarity 75.7%; Pred. No. 23;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy      4 ATACCTACTCCAAACAAATCCATCTTACTCATGCAAC 40
Db      2052 ATACCACCTACCAACCAAGTCAAGCTTATTGATGCAAC 2088

RESULT 4
US-09-925-065A-591011/c
; Sequence 591011, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 591011
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-591011

Query Match      55.5%; Score 22.2; DB 6; Length 611;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      14 CCAACAAATCCATCTTACTCATGCAAC 40
Db      351 CCAACAAACCACTTACTCATGCAAC 325

RESULT 5
US-09-925-065A-591012/c
; Sequence 591012, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 591012
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-591012

Query Match      55.5%; Score 22.2; DB 6; Length 611;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      14 CCAACAAATCCATCTTACTCATGCAAC 40
Db      351 CCAACAAACCACTTACTCATGCAAC 325

RESULT 6
US-09-925-065A-591013/c
; Sequence 591013, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 591013
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-591013
```

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 591013
LENGTH: 611
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-591013

Query Match 55.5%; Score 22.2; DB 6; Length 611;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 14 CCAACAATCCATCTTACTCATGCAAC 40
Db 351 CCAACAACACCTTACTCATGCGC 325

RESULT 7
US-09-925-065A-253727
Sequence 253727, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 253727
LENGTH: 613
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-253727

Query Match 55.5%; Score 22.2; DB 6; Length 613;
Best Local Similarity 73.0%; Pred. No. 22;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 2 GGATCTACTCCCAACATCCATCTTACTCATGCA 38
Db 292 GGAACTCACTCCCAACATCCATCTTACTCATGCA 328

RESULT 8
US-09-925-065A-888321/c

Sequence 888321, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 888321
LENGTH: 628
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-888321

Query Match 55.0%; Score 22; DB 6; Length 628;
Best Local Similarity 73.7%; Pred. No. 27;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 GGATCTACTCCCAACATCCATCTTACTCATGCA 39
Db 224 GGAACTCACTCCCAACATCCATCTTACTCATGCA 187

RESULT 9
US-09-925-065A-393490/c
Sequence 393490, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 393490
LENGTH: 598
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-393490

Query Match 54.0%; Score 21.6; DB 6; Length 598;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 TACTCTACTCCCAACATCCATCTTACT 32
Db 228 TATCTCTCTCAATCAATCAATCTTACT 201

```
RESULT 10
US-09-925-065A-281837
; Sequence 281837, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281837
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-281837

Query Match      53.5%; Score 21.4; DB 6; Length 560;
Best Local Similarity 71.8%; Pred. No. 46;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 1 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAA 39
|||||
Db 373 AGGAATCACTCCAAAGGAACCTCGAACCCATGCAA 411

RESULT 11
US-09-925-065A-281838
; Sequence 281838, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281838
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-281838

Query Match      53.5%; Score 21.4; DB 6; Length 560;
Best Local Similarity 71.8%; Pred. No. 46;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 1 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAA 39
|||||
Db 373 AGGAATCACTCCAAAGGAACCTCGAACCCATGCAA 411

RESULT 12
US-09-925-065A-189248/c
; Sequence 189248, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189248
; LENGTH: 620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-189248

Query Match      53.5%; Score 21.4; DB 6; Length 620;
Best Local Similarity 75.8%; Pred. No. 47;
Matches 25; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Oy 1 AGGTACTACTCCCAACAAATCCATCTTACTC 33
|||||
Db 175 ATGATACCTACTTCCTATCTATGATCTCACTC 143

RESULT 13
US-09-925-065A-63167
; Sequence 63167, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63167
; LENGTH: 653
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-63167

Query Match      53.5%; Score 21.4; DB 6; Length 653;
Best Local Similarity 71.8%; Pred. No. 47;
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us-10-713-381-1_copy_1239_1278.rnpbn

Wed Mar 8 14:17:00 2006

Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 4 ATACCTACTCCCAACCAATCCATCTTACTCATGCAAC 40
 DB 387 ATACCTACTCCCAACCAATCCATCTTACTCATGCAAC 423
 Search completed: March 6, 2006, 10:32:45
 Job time : 41.7555 secs

Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 QY 1 AGGATACCTACTCCCAACCAATCCATCTTACTCATGCA 39
 DB 186 AGGAAACCTACACCTGACATGTCAACTAATCACTGCA 224

RESULT 14
 US-11-124-367A-24503
 ; Sequence 24503, Application US/11124367A
 ; Publication No. US20060024700A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michele Cargill
 ; TITLE OF INVENTION: Genetic Polymorphisms Associated with
 ; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
 ; FILE REFERENCE: CL001519.ORD
 ; CURRENT APPLICATION NUMBER: US/11/124,367A
 ; CURRENT FILING DATE: 2005-05-09
 ; PRIOR APPLICATION NUMBER: US 60/568,846
 ; PRIOR FILING DATE: 2004-05-07
 ; PRIOR APPLICATION NUMBER: US 60/582,609
 ; PRIOR FILING DATE: 2004-06-25
 ; PRIOR APPLICATION NUMBER: US 60/599,554
 ; PRIOR FILING DATE: 2004-08-09
 ; NUMBER OF SEQ ID NOS: 34460
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 24503
 ; LENGTH: 201
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-11-124-367A-24503
 Query Match 52.5%; Score 21; DB 12; Length 201;
 Best Local Similarity 73.0%; Pred. No. 52;
 Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 GATACCTACTCCCAACCAATCCATCTTACTCATGCA 39
 DB 43 GATACCTGTCTCAAAAATACATATTAAACATTTAA 79

RESULT 15
 US-09-925-065A-285326
 ; Sequence 285326, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827/115
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; CURRENT FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: US 60/243,096
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 60/252,147
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR APPLICATION NUMBER: US 60/250,092
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: US 60/261,766
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289,846
 ; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 285326
 ; LENGTH: 617
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-09-925-065A-285326
 Query Match 52.5%; Score 21; DB 6; Length 617;
 Best Local Similarity 73.0%; Pred. NO. 68;

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